

10B15

## SEARCH REQUEST FORM

5-475

## Requestor's

Name: John Wm

## Serial

Number: 08/918874

Date: 5-14-98

Phone: 308-4008

Art Unit: 1646

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please send SEQ ID No: 1 + 2  
of 08/918874.

## STAFF USE ONLY

Date completed: 5/18  
Searcher: 88308-429

Terminal time: 5

Elapsed time: Preps

CPU time:

Total time:

Number of Searches:

Number of Databases: 7

## Search Site

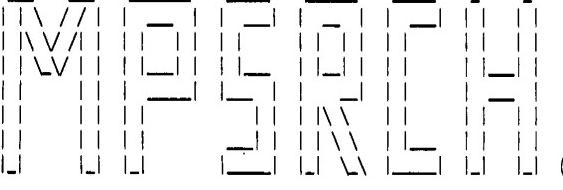
 STIC CM-1 Pre-S

## Type of Search

 N.A. Sequence A.A. Sequence Structure Bibliographic

## Vendors

 IG Suite STN Dialog APS Geninfo SDC DARC/Questel Other MPArch

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Release 3.0.5AA John F. Collins, Biocomputing Research Unit.  
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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri May 15 17:45:22 1998; MasPar time 2128.68 Seconds  
 1495.787 Million cell updates/sec

Tabular output not generated.

Title: >US-08-918-874-2  
 Description: (1-2082) from US08918874.seq  
 Perfect Score: 2082

N.A. Sequence: 1 CCAAATGCACCTCGGTTCTA.....CATTTTATATTGCTTTACTA 2082  
 Comp: GGTTGACGTGGAGCCAAGAT.....GTAAAAATAAACGAATGAT

Scoring table: TABLE default  
 Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: embl53  
 1:em\_in 2:em\_or 3:em\_om 4:em\_ov 5:em\_pl 6:em\_htg  
 7:em\_hum1 8:em\_hum2 9:em\_ba 10:em\_ro 11:em\_un 12:em\_v1  
 13:em\_pat

Database: genbank105  
 14:gb\_ro 15:gb\_om 16:gb\_ov 17:gb\_in 18:gb\_pl 19:gb\_ba  
 20:gb\_st 21:gb\_v1 22:gb\_ph 23:gb\_sy 24:gb\_un 25:gb\_pat  
 26:gb\_htg 27:gb\_pr1 28:gb\_pr2

Statistics: Mean 11.767; Variance 5.428; scale 2.168

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query						
No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1776	85.3	1804	28	AF029761	Homo sapiens decoy rec	0.00e+00
2	1161	55.8	1161	28	AF023849	Homo sapiens TNF recep	0.00e+00
3	390	18.7	1180	28	AF012536	Homo sapiens decoy rec	0.00e+00
4	390	18.7	1377	28	AF033854	Homo sapiens lymphocyt	0.00e+00
5	388	18.6	900	28	AF020502	Homo sapiens cytotoxic	0.00e+00
6	386	18.5	1388	28	AF016267	Homo sapiens TRAIL rec	0.00e+00
7	345	16.6	780	28	AF012629	Homo sapiens antagonist	1.22e-273
8	264	12.7	1323	28	AF018658	Homo sapiens apoptosis	3.16e-200
9	265	12.7	3993	28	AF016266	Homo sapiens TRAIL rec	3.97e-201
10	259	12.4	1859	28	AF016849	Homo sapiens apoptosis	1.01e-195
11	202	9.7	1407	28	HSU90875	Human cytotoxic ligand	1.06e-144
12	195	9.4	1236	28	AF020501	Homo sapiens cytotoxic	1.75e-138
13	195	9.4	1236	28	AF018657	Homo sapiens apoptosis	1.75e-138
14	196	9.4	1717	28	AF016268	Homo sapiens death rec	2.27e-139

15	194	9.3	1799	28	AF012535	Homo sapiens death rec	1.35e-137	
16	191	9.2	1236	28	AF012628	Homo sapiens death dom	6.14e-135	
17	191	9.2	1235	28	AF022386	Homo sapiens p53-regul	6.14e-135	
18	96	4.6	92975	28	AC002369	Homo sapiens Xp22 PAC	8.54e-53	
19	93	4.5	99207	28	HS102G20	Human DNA sequence fro	2.63e-50	
20	93	4.5	148451	26	AC004031	Homo sapiens; HTGS pha	2.63e-50	
21	93	4.5	149490	28	HSU95740	Human chromosome 16p13	2.63e-50	
22	94	4.5	173767	28	AC002449	Human PAC clone DJ404K	3.90e-51	
c	23	92	4.4	63369	26	AC002413	*** SEQUENCING IN PROG	1.77e-49
c	24	92	4.4	91690	28	HS96A9	Human DNA sequence fro	1.77e-49
c	25	91	4.4	153460	28	HSU52111	Homo sapiens Xq28 geno	1.18e-48
c	26	92	4.4	165279	26	HS26D12	Human DNA sequence ***	1.77e-49
c	27	89	4.3	15913	28	HSALADG	H.sapiens ALAD gene fo	5.25e-47
c	28	90	4.3	34352	28	U73638	Human Chromosome 11 Co	7.89e-48
c	29	89	4.3	40491	28	AC002116	Human DNA from chromos	5.25e-47
c	30	89	4.3	93273	28	AC004084	Homo sapiens BAC clone	5.25e-47
c	31	90	4.3	139034	26	HS508I15	Human DNA sequence ***	7.89e-48
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c	33	90	4.3	145717	26	HS108K11	Human DNA sequence ***	7.89e-48
c	34	89	4.3	145831	28	HSAF001548	Homo sapiens chromosom	5.25e-47
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c	39	88	4.2	40145	28	HSL19H1	Human DNA sequence fro	3.49e-46
c	40	88	4.2	43726	26	HSN102C10	Human DNA sequence ***	3.49e-46
c	41	88	4.2	80168	28	HSAC002078	Human BAC clone RG111H	3.49e-46
c	42	88	4.2	114411	28	HUAC02551	Homo sapiens Chromosom	3.49e-46
c	43	88	4.2	172984	28	HSU91318	Human chromosome 16p13	3.49e-46
c	44	88	4.2	179544	28	AF015720	Homo sapiens chromosom	3.49e-46
c	45	88	4.2	219447	27	HUMFLNG6PD	Homo sapiens chromosom	3.49e-46

#### ALIGNMENTS

RESULT	LOCUS	DEFINITION	JOURNAL	REFERENCE	FEATURES
1	AF029761	Homo sapiens decoy receptor 2 mRNA, complete cds.	Curr. Biol. (1997) In press	1 (bases 1 to 1804)	source
		AF029761		Marsters,S.A., Sheridan,J.P., Pitti,R.M., Huang,A., Skubatch,M., Baldwin,D., Yuan,J., Gurney,A., Goddard,A.D., Godowski,P. and Ashkenazi,A.	
		g2688980		A Novel Receptor for Apo2L/TRAIL Contains a Truncated Death Domain	
				Primates; Catarrhini; Hominidae; Homo.	
				1 (bases 1 to 1804)	
				Marsters,S.A., Sheridan,J.P., Pitti,R.M., Huang,A., Skubatch,M., Baldwin,D., Yuan,J., Gurney,A., Goddard,A.D., Godowski,P. and Ashkenazi,A.	
				Curr. Biol. (1997) In press	
				2 (bases 1 to 1804)	
				Marsters,S.A., Sheridan,J.P., Pitti,R.M., Huang,A., Skubatch,M., Baldwin,D., Yuan,J., Gurney,A., Goddard,A.D., Godowski,P. and Ashkenazi,A.	
				Submitted (14-OCT-1997) Molecular Oncology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA	
					Location/Qualifiers
					source
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					/map="8p21"
					161..1321
					/function="inhibitory receptor for Apo2L/TRAIL"
					/note="DCR2; member of the TNF receptor superfamily that contains a truncated death domain"
					/codon_start=1
					/product="decoy receptor 2"
					/db_xref="PID:g2688981"
					/translation="MGLWGQSVPASSARAGRYPGARTASGTRPWLLDPKILKFVVFI

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BASE COUNT 454 a 462 c 460 g 428 t  
 ORIGIN

Query Match 85.3%; Score 1776; DB 28; Length 1804;  
 Best Local Similarity 99.7%; Pred. No. 0.00e+00;  
 Matches 1799; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

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 Qy 1 CCAAATGCCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGAC 60  
 Db 61 CTCGACCCACCGTCCGGCAGAACCTTGCACGCCACAAACTACGGGAGCATTCTG 120  
 Qy 61 CTCGACCCACCGTCCGG---AACCTTGCACGCCACAAACTACGGGAGCATTCTG 116  
 Db 121 ATTGATTTTGGCGTTTCGATCCACCTCCCTCTCATGGACTTTGGGACAAG 180  
 Qy 117 ATTGATTTTGGCGTTTCGATCCACCTCCCTCTCATGGACTTTGGGACAAG 176  
 Db 181 CGTCCCAGCCGCTCGAGCGCTCGAGCAGGGCGTATCCAGGAGGCCAGGACAGCGTCGGG 240  
 Qy 177 CGTCCCAGCCGCTCGAGCGCTCGAGCAGGGCGTATCCAGGAGGCCAGGACAGCGTCGGG 236  
 Db 241 AACCAAGACCATGGCTCTGGACCCCAAGATCTTAAGTCGTGCTCTCATCGTCGGG 300  
 Qy 237 AACCAAGACCATGGCTCTGGACCCCAAGATCTTAAGTCGTGCTCTCATCGTCGGG 296  
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 Qy 297 TCTGCTCCGGTCCGGGTTGACTCTGCCACCATCCCCGGCAGGACAGTTCCCAGCA 356  
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 Db 781 CTCTCCCTATCACTACCTTATCATCATAGTGGTTTAGTCATCTTAGTGTGGTGT 840  
 Qy 777 CTCTCCCTATCACTACCTTATCATCATAGTGGTTTAGTCATCTTAGTGTGGTGT 836  
 Db 841 GGTGGCTTTCATGTCGGAAGAAATTCAATTCTTACCTCAAGGCATCTGTCAGGTGG 900  
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 Qy 1137 GAGGAGGAGGCTGCTGGTTCACTGATGACGCTGACTCCGCTGACATCAGCACCTTGCT 1196  
 Db 1201 GGATGCCCTCGAACACTGAAAGAAGGACATGCAAAGGAACAATTCAAGGACCAACTGGT 1260  
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 Db 1801 CTCT 1804  
 Qy 1797 CTCT 1800

RESULT 2  
 LOCUS AF023849 1161 bp mRNA PRI 01-DEC-1997  
 DEFINITION Homo sapiens TNF receptor-related receptor for TRAIL mRNA, complete cds.  
 ACCESSION AF023849  
 NID g2653844  
 KEYWORDS .

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1161)  
 AUTHORS Pan,G.  
 TITLE TRUNDD, a new member of the TRAIL receptor family that antagonizes  
 TRAIL signalling  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1161)  
 AUTHORS Pan,G., Ni,J. and Dixit,V.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-SEP-1997) Pathology, University of Michigan, 1301  
 Catherine Road, MSRB1, RM7520, Ann Arbor, MI 48109, USA  
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BASE COUNT 290 a 301 c 328 g 242 t  
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Query Match 55.8%; Score 1161; DB 28; Length 1161;  
 Best Local Similarity 99.9%; Pred. No. 0.00e+00;  
 Matches 1160; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 Db 121 GTCGCTTTCATCGCGGTCTGCTGCCGTTGACTCTGCCACATCCCCGG 180  
 Qy 277 GTCGCTTTCATCGCGGTCTGCTGCCGTTGACTCTGCCACATCCCCGG 336  
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 Qy 457 GAGGGTGTGGATTACACCATTGCTCCAACAATTGCTTCTTGCTGTATGACAGTT 516  
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 Qy 517 TGTAAATCAGGTCAAACAAATAAAAGTCTGTACCGACCCAGAGACACCGTGTCAAG 576  
 Db 421 TGTAAAAAGGAAGCTCCAGGATAAAAACCTCCCTGAGATGTGCCGGACGTGAGAAC 480  
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 Qy 637 GGGTGTCCCAGAGGGATGGTCAAGGTCAAGTAAATTGTACGCCCGGAGTGACATCAAGTGC 696

Db 541 AAAATGAATCAGCTGCCAGTCCACTGGAAAACCCAGCAGCGGAGGAGACAGTGAC 600  
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 Qy 817 ATCATTTAGCTGTGGTTGGCTTTCATGCGAGAAATCATTCTTACCTC 876  
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 Db 1141 TCTGCTACGTCTGCCGTGTA 1161  
 Qy 1297 TCTGCTACGTCTGCCGTGTA 1317

RESULT	3	LOCUS	AF012536	1180 bp	mRNA	PRI	21-AUG-1997
DEFINITION	Homo sapiens decoy receptor 1 (DcR1) mRNA, complete cds.						
ACCESSION	AF012536						
NID	g2338421						
KEYWORDS	human.						
SOURCE	Homo sapiens						
ORGANISM	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 1180)						
AUTHORS	Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Skubatch,M., Baldwin,D., Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I., Goddard,A.D., Godowski,P. and Ashkenazi,A.						
TITLE	Control of TRAIL-induced apoptosis by a family of signaling and decoy receptors						
JOURNAL	Science 277 (5327), 818-821 (1997)						
MEDLINE	97390509						
REFERENCE	2 (bases 1 to 1180)						
AUTHORS	Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Baldwin,D., Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I., Goddard,A.D., Godowski,P. and Ashkenazi,A.						
TITLE	Direct Submission						
JOURNAL	Submitted (06-JUL-1997) Molecular Oncology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA						

FEATURES	Location/Qualifiers	DEFINITION	Homo sapiens lymphocyte inhibitor of TRAIL (LIT) mRNA, complete cds.
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CDS	193. .972 /gene="DcR1" /note="tumor necrosis factor receptor family member; inhibits apoptosis induction by TRAIL/Apo2L" /codon_start=1 /product="decoy receptor 1" /db_xref="PID:g2338422" /translation="MARIPTKLKFVVIVAVLLPVLA SATTARQEEVPPQQTVAPOQQ RHFSKGECECPAGSHRSRSEHTGACNPCTEGVDYTNASNNEPSCFCVCKSDQKHSSCT MTRDTVCQCKEGRNENSPEMCRKCSRCPSPGEVQVSNCSTSDDIQCVEFGANATIVE TPAAAEETMTNSPGTPAPAAEETMTNSPGTPAPAAEETMTNSPGTPAPAAEETMTNSPG TPAPAAEETMTNSPGTPASSHYLSCTIVGIIVLIVLLIVFV"	KEYWORDS	.
BASE COUNT	338 a 326 c 298 g 218 t	SOURCE	human.
ORIGIN		ORGANISM	Homo sapiens
Query Match	18.7%; Score 390; DB 28; Length 1180;	DEFINITION	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Best Local Similarity	83.5%; Pred. No. 0.00e+00;	REFERENCE	1 (bases 1 to 1377)
Matches	517; Conservative 0; Mismatches 97; Indels 5; Gaps 4;	AUTHORS	Mongkolsapaya,J., Cowper,A., Xu,X., Morris,G., McMichael,A.J., Bell,J.I. and Scream, G.R.
Db	107 GGAAC TCTGGGACAGAGCGCCCCCGCCCT-GATGGCCGAGGCAGGGTGCACCCAGG 165 	TITLE	Lymphocyte inhibitor of TRAIL: A new receptor protecting lymphocytes from the death ligand TRAIL
Qy	159 GGGACTTGGGACAAAGCGTCCCAGCCGCTCGAGCAGGGCCTATCCAGG 218	JOURNAL	J. Immunol. (1997) In press
Db	166 ACCCAGGACGGCTGGGAACCATAACCATGGC-CGGATCCCCAAGACCCCTAAAGTTCT 224 	REFERENCE	2 (bases 1 to 1377)
Qy	219 AGCCAGGACAGCGTCGGAACCAAGACCATGGCTCTGGACCCCCAAGATCCTTAAGTTCT 278	AUTHORS	Mongkolsapaya,J., Cowper,A., Xu,X., Morris,G., McMichael,A.J., Bell,J.I. and Scream, G.R.
Db	225 CGTCTGCATCGTCGGTCTGCTGCCAGTCAGCTACTCTGCCACCACTGCCCGCA 284 	TITLE	Direct Submission
Qy	279 CGTCTGCATCGTCGGTCTGCTGCCGGTCCGGGTGACTCTGCCACCATCCCCGGCA 338	JOURNAL	Submitted (10-NOV-1997) Immunology, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DS, UK
Db	285 GGAGGAAGTCCCCAGCACAGTCGGCCCCACAGCAACAGAGCACAGCTCAAGGGGA 344 	FEATURES	Location/Qualifiers
Qy	339 GGACGAAGTCCCCAGCACAGTCGGCCCCACAGCAACAGAGGCGCAGGCCCAAGGAGGA 398	source	1. .1377
Db	345 GGAGTGTCCAGCAGGATCTCATAGATCAGAACATACTGGCCCTGTAACCGTGACAGA 404 	/organism="Homo sapiens"	
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Db	405 GGGTGTGATTACACCAACGCTTCCAACAATGAACCTTCTTGCTTCCATGTACAGTTG 464 	/cell_type="lymphocyte"	
Qy	459 GGGTGTGATTACACCATTGCTTCCAACAATTGCTTCTTGCCCTGCTATGTACAGTTG 518	gene	1. .1377
Db	465 TAAATCAGATCAAAACATAAAAGTCTCTGCACCATGACCAGAGACACAGTGTCTAGTG 524 	/gene="LIT"	
Qy	519 TAAATCAGGTCAAACAATAAAAGTCTCTGACACGAGAGACACCGTGTCTAGTG 578	CDS	177. .956
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Qy	579 TAAAAAAGGAAGCTTCAGGATAAAAACCTCCCTGAGATGTGCCGAAGTGTAGAACAGG 638	/codon_start=1 /product="lymphocyte inhibitor of TRAIL" /db_xref="PID:g2645842" /translation="MARIPTKLKFVVIVAVLLPVLA SATTARQEEVPPQQTVAPOQQ RHFSKGECECPAGSHRSRSEHTGACNPCTEGVDYTNASNNEPSCFCVCKSDQKHSSCT MTRDTVCQCKEGRNENSPEMCRKCSRCPSPGEVQVSNCSTSDDIQCVEFGANATIVE TPAAAEETMTNSPGTPAPAAEETMTNSPGTPAPAAEETMTNSPGTPAPAAEETMTNSPG TPAPAAEETMTNSPGTPASSHYLSCTIVGIIVLIVLLIVFV"	
BASE COUNT	335 a 409 c 365 g 268 t	BASE COUNT	335 a 409 c 365 g 268 t
ORIGIN		ORIGIN	
Query Match	18.7%; Score 390; DB 28; Length 1377;	Query Match	18.7%; Score 390; DB 28; Length 1377;
Best Local Similarity	83.5%; Pred. No. 0.00e+00;	Best Local Similarity	83.5%; Pred. No. 0.00e+00;
Matches	517; Conservative 0; Mismatches 97; Indels 5; Gaps 4;	Matches	517; Conservative 0; Mismatches 97; Indels 5; Gaps 4;
Db	91 GGAAC TCTGGGACAGAGCGCCCCCGCCCT-GATGGCCGAGGCAGGGTGCACCCAGG 149 	Db	91 GGAAC TCTGGGACAGAGCGCCCCCGCCCT-GATGGCCGAGGCAGGGTGCACCCAGG 149 
Qy	159 GGGACTTGGGACAAAGCGTCCCAGCCGCTCGAGCAGGGCCTATCCAGG 218	Qy	159 GGGACTTGGGACAAAGCGTCCCAGCCGCTCGAGCAGGGCCTATCCAGG 218
Db	150 ACCCAGGACGGCTGGGAACCATAACCATGGC-CGGATCCCCAAGACCCCTAAAGTTCT 208 	Db	150 ACCCAGGACGGCTGGGAACCATAACCATGGC-CGGATCCCCAAGACCCCTAAAGTTCT 208 
Qy	219 AGCCAGGACAGCGTCGGAACAGACCATGGCTCTGGACCCCCAAGATCCTTAAGTTCT 278	Qy	219 AGCCAGGACAGCGTCGGAACAGACCATGGCTCTGGACCCCCAAGATCCTTAAGTTCT 278
Db	209 CGTCTGCATCGTCGGTCTGCTGCCAGTCAGCTACTCTGCCACCACTGCCCGCA 268 	Db	209 CGTCTGCATCGTCGGTCTGCTGCCAGTCAGCTACTCTGCCACCACTGCCCGCA 268 
Qy	279 CGTCTGCATCGTCGGTCTGCTGCCGGTTGACTCTGCCACCATCCCCGGCA 338	Qy	279 CGTCTGCATCGTCGGTCTGCTGCCGGTTGACTCTGCCACCATCCCCGGCA 338
Db	269 GGAGGAAGTCCCCAGCACAGTCAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGA 328 	Db	269 GGAGGAAGTCCCCAGCACAGTCAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGA 328 
Qy	339 GGACGAAGTCCCCAGCACAGTCAGTGGCCCCACAGCAACAGAGGCGCAGGCCCAAGGAGGA 398	Qy	339 GGACGAAGTCCCCAGCACAGTCAGTGGCCCCACAGCAACAGAGGCGCAGGCCCAAGGAGGA 398
Db	329 GGAGTGTCCAGCAGGATCTCATAGATCAGAACATACTGGCCCTGTAACCGTGACAGA 388 	Db	329 GGAGTGTCCAGCAGGATCTCATAGATCAGAACATACTGGCCCTGTAACCGTGACAGA 388 
Qy	399 GGAGTGTCCAGCAGGATCTCATAGATCAGAACATACTGGCCCTGTAACCGTGACAGA 458	Qy	399 GGAGTGTCCAGCAGGATCTCATAGATCAGAACATACTGGCCCTGTAACCGTGACAGA 458
Db	389 GGGTGTGATTACACCAACGCTTCCAACAATGAACCTTCTTGCTTCCATGTACAGTTG 448 	Db	389 GGGTGTGATTACACCAACGCTTCCAACAATGAACCTTCTTGCTTCCATGTACAGTTG 448 
Qy	459 GGGTGTGATTACACCATTGCTTCCAACAATTGCTTCTTGCCCTGCTATGTACAGTTG 518	Qy	459 GGGTGTGATTACACCATTGCTTCCAACAATTGCTTCTTGCCCTGCTATGTACAGTTG 518
Db	449 TAAATCAGATCAAAACATAAAAGTCTCTGCACCATGACCAGAGACACAGTGTCTAGTG 508 	Db	449 TAAATCAGATCAAAACATAAAAGTCTCTGCACCATGACCAGAGACACAGTGTCTAGTG 508 

RESULT 4  
LOCUS AP033854 1377 bp mRNA PRI 27-NOV-1997

Qy 519 TAAATCAGGTCAAACAATAAAGTCCCTGACCACAGAGACACCGTGTCAGTG 578  
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 Qy 579 TGAAAAGGAAGCTCCAGATAAAAACCTCCCTGAGATGTGCCGGAGTGTAGAACAGG 638  
 Db 567 -TGCCCTAGTGGGAAGTCCAAGTCAGTAATTGTACCTCTGGATGATATCCAGTGT 625  
 Qy 639 GTGTCCCAGAGGGATGGTCAAGTCAGTAATTGTACCCCCGGAGTGACATCAAGTGCAA 698  
 Db 626 TGAAGAATTGGTCCAATGCCACTGTGGAAACCCCAGCTGCTGAAGAGAACATGAACAC 685  
 Qy 699 AAATGAATCAGCTGCCAGTTCCACTGGAAAACCCACAGCGGGAGGAGACACTGACAC 758  
 Db 686 CAGCCGGGGACTCCTGCC 704  
 Qy 759 CATCCTGGGATGCTTGCC 777

**RESULT** 5  
**LOCUS** AF020502 900 bp mRNA **PRI** 28-SEP-1997

**DEFINITION** Homo sapiens cytotoxic TRAIL receptor-3 (TRAIL-R3) mRNA, complete cds.

**ACCESSION** AF020502  
**NID** g2443819  
**KEYWORDS**.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 900)  
**AUTHORS** MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T., Cohen,G.M. and Alnemri,E.S.  
**TITLE** Identification and Molecular Cloning of Two Novel Receptors for the Cytotoxic ligand TRAIL  
**JOURNAL** J. Biol. Chem. (1997) In press  
**REFERENCE** 2 (bases 1 to 900)  
**AUTHORS** MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T., Cohen,G.M. and Alnemri,E.S.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (21-AUG-1997) Department of Microbiology and Immunology, Kimmel Cancer Institute, 233 S. 10th Street, Philadelphia, PA 19107, USA

**FEATURES**

<b>source</b>	Location/Qualifiers
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	/organism="Homo sapiens"
	/db_xref="taxon:9606"
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<b>gene</b>	1. .900
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<b>CDS</b>	1. .900
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**BASE COUNT** 228 a 262 c 240 g 170 t  
**ORIGIN**

Query Match 18.6%; Score 388; DB 28; Length 900;  
 Best Local Similarity 83.4%; Pred. No. 0.0e+00;  
 Matches 516; Conservative 0; Mismatches 98; Indels 5; Gaps 4;

Db 35 GGAACCTGGGACAGAGCGCCCCGGCGCCT-GATGGCCGAGGCAGGGTGCAGCCCAGG 93  
 Qy 159 GGGACTTGGGACAAAGCGTCCCACCGCCTGAGCGCTGAGCAGGGCCTATCCAGG 218  
 Db 94 ACCCAAGACGGCGTGGGAACCATACCATGGC-CCGGATCCCCAAGACCTAAAGTCG 152  
 Qy 219 AGCCAGGACAGCGTGGGAACCATGGCTCTGGACCCCAAGATCCCTAAGTCG 278  
 Db 153 CGTGTCTATCGTCGGGCTCTGCTGCCAGTCTACTCTGCCACCACTGCCGGCA 212  
 Qy 279 CGTCTTCATCGTCGGGTTCTGCTGCCGGTCCGGGTGACTCTGCCACCATCCCCGGCA 338  
 Db 213 GGAGGAAGTTCCCCAGCAGACAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGA 272  
 Qy 339 GGACGAAGTTCCCCAGCAGACAGTGGCCCCACAGCAACAGAGGCACGCCCTCAAGGAGGA 398  
 Db 273 GGACTGTCCAGCAGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCGTCAACAGA 332  
 Qy 399 GGAGTGTCCAGCAGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCGTCAACAGA 458  
 Db 333 GGGTGTGATTACACCAACGCTTCAACAATGAACCTTCTGCTTCCATGTACAGTTG 392  
 Qy 459 GGGTGTGATTACACCAACGCTTCAACAATTTGCTCTGCTGCTATGTACAGTTG 518  
 Db 393 TAAATCAGATAAAAACATAAAAAGTCTGCCACATGACCAGAGACAGTGTGTCAGTG 452  
 Qy 519 TAAATCAGGTCAAACAATAAAAGTCTGCTGACAGCAGAGACACCGTGTGTCAGTG 578  
 Db 453 TAAAGAAGGCACCTCCGGAAATGAAAACCTCCAGAGATGTGCCGGAGTGTAG--CAGG 510  
 Qy 579 TGAAAAGGAAGCTCCAGGATAAAAACCTCCCTGAGATGTGCCGGAGTGTAGAACAGG 638  
 Db 511 -TGCCCTAGTGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGATGATATCCAGTGT 569  
 Qy 639 GTGTCCCAGAGGGATGGTCAAGTCAGTAATTGTACGCCGGAGTGACATCAAGTGCAA 698  
 Db 570 TGAAGAATTGGTCCAATCCACTGTGGAAACCCCAGCTGCTGAAGAGACAATGAACAC 629  
 Qy 699 AAATGAATCAGCTGCCAGTCCACTGGAAAACCCAGCAGCGGGAGGAGACAGTGCAC 758  
 Db 630 CAGCCGGGGACTCCTGCC 648  
 Qy 759 CATCCTGGGATGCTTGCC 777

**RESULT** 6  
**LOCUS** AF016267 1388 bp mRNA **PRI** 16-OCT-1997

**DEFINITION** Homo sapiens TRAIL receptor 3 mRNA, complete cds.

**ACCESSION** AF016267  
**NID** g2529564  
**KEYWORDS**.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 1388)  
**AUTHORS** Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and Tschopp,J.  
**TITLE** Characterization of two receptors binding TRAIL  
**JOURNAL** FEBS Lett. (1997) In press  
**REFERENCE** 2 (bases 1 to 1388)  
**AUTHORS** Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and Tschopp,J.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (28-JUL-1997) Institute of Biochemistry, University of Lausanne, Chemin des Boveresses 155, Epalinges, VD 1066, Switzerland

**FEATURES**

<b>source</b>	Location/Qualifiers
	1. .1388
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	/db_xref="taxon:9606"



Qy 738 AGCGGAGGAGACAGTGACCACCATCCTGGGGATGCTGCC 777

RESULT 8  
 LOCUS AF018658 1323 bp mRNA PRI 18-SEP-1997  
 DEFINITION Homo sapiens apoptosis inducing protein (TRICK2B) mRNA, complete cds.  
 ACCESSION AF018658  
 NID g2407652  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1323)  
 AUTHORS Scream, G.R., Mongkolsapaya, J., Xu, X., Cowper, A.E., McMichael, A.J. and Bell, A.J.  
 TITLE TRICK2 a new alternatively spliced receptor which transduces the cytotoxic signal from TRAIL  
 JOURNAL Curr. Biol. (1997) In press  
 REFERENCE 2 (bases 1 to 1323)  
 AUTHORS Scream, G.R., Mongkolsapaya, J., Xu, X., Cowper, A.E., McMichael, A.J. and Bell, A.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-AUG-1997) Molecular Immunology, Institute of Molecular Medicine, Oxford University, John Radcliffe Hospital, Headington, Oxford OX3 9DS, UK  
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 /db\_xref="taxon:9606"  
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 CDS 1..1323  
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 /note="alternatively spliced; similar to TNF receptor; contains 2 TNF-R repeats and cytoplasmic death domain"  
 /codon\_start=1  
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 /note="putative retained intron; consensus splice sites at both ends"  
 BASE COUNT 319 a 343 c 397 g 264 t  
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 Best Local Similarity 68.6%; Pred. No. 3.16e-200;  
 Matches 705; Conservative 1; Mismatches 298; Indels 24; Gaps 17;

Db 1 ATGGAACACGGGGACAGAACGCCCGCCGTTGGGGCCGAAAGGCACGGCCA 60  
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 Qy 157 ATGGGACTTTGGGGACAAAGCGTCCGACCGCCTCGAGCGCTCGAGCAGGGCTATCCA 216  
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 Db 61 GGACCCAGGGAGGCCGGGGAGCCAGGCGCTGGGCTCGGGTCCCCAAGACCCCTT--GTGC 118  
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 Qy 217 GGAGCCAGGACAGCGTCGGGAACCCAGACCATGGCTCTGGACCCCAAGATCCTTAAGTTC 276  
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 Db 119 -TCGT--TG-TCGCCCGGGTCTGCTGTTGGCTCAAGCTGAGTCTGCTCTGATCACCAA 174  
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 Qy 277 GTCGTCTCATCGTCGCGGTTCTGCTGCCGGTCCGGGTGACTCTGCCACCATCCCCGG 336  
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 Db 175 CAAGACCTAGCTCCCCAGCAGAGAGTGGCCCCACAACAAAAGAGGTCCAGCCCCCTCAGAG 234

Qy 337 CAGGACGAAGTCCCACGCAGACAGTGCCCCACAGCAACAGAGGCCAGCCTCAAGGAG 396  
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 Db 769 CGTGTG-GA-CAGAACCT-CACAACGACCTGGGCTGAGGACAATGCTCAATGAGATC 825  
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 Qy 934 CGCGGGCGTCATGTCCTCACGACTTCTGGGGAGGACATCCCGCAACGAGAC 993  
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 Db 826 GTGAGTA----T-CTTGAGCCACCCAGGTCTGAGCAGGAAATGGAAGTCCAGG 879  
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 Qy 994 CTGAGTAACAGATACTTGCAGCCCACCCAGGTCTGAGCAGGAAATCCAAGGTCAAGG 1053  
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 Qy 1054 CTGGCAGACTAACAGGTGTCAGTGTAGACTYCCAGAGGAGCCACCGCTCTGCTGAA 1113  
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 Db 1000 CCCACTGA 1007  
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 Qy 1174 TCCGCTGA 1181

RESULT 9  
 LOCUS AF016266 3993 bp mRNA PRI 16-OCT-1997  
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 ACCESSION AF016266  
 NID g2529562  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 3993)  
 AUTHORS Schneider, P., Bodmer, J.-L., Thome, M., Holler, N., Hofmann, K. and

**TITLE** Characterization of two receptors binding TRAIL  
**JOURNAL** FEBS Lett. (1997) In press  
**REFERENCE** 2 (bases 1 to 3993)  
**AUTHORS** Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and Tschopp,J.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (28-JUL-1997) Institute of Biochemistry, University of Lausanne, Chemin des Boveresses 155, Epalinges, VD 1066, Switzerland  
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**CDS** 118..1440  
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BASE COUNT      961 a    964 c    1014 g   1052 t     2 others
ORIGIN

Query Match      12.7%; Score 265; DB 28; Length 3993;
Best Local Similarity  68.6%; Pred. No. 3.97e-201;
Matches 706; Conservative 1; Mismatches 298; Indels 24; Gaps 17;

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Db	117	CATGGAAACACGGGAGCAGAACGCCCGGCGCTTCGGGGCCCGAAAAGGCACGGCCC 176
Qy	156	CATGGGACTTGGGACAAAGCGTCCGACCGCTCGAGCGCTCGAGCAGGGCGTATCC 215
Db	177	AGGACCCAGGGAGGCCGGGGAGCCAGGCCCTGGCTCCGGTCCCCAAGACCCCTT-GTG 234
Qy	216	AGGAGCCAGGACACCGTCGGAACCGACCATGGCTCTGGACCCCCAAGATCTTAAGT 275
Db	235	C-TCGT--TG-TCCGGCGGTCTCTGCTGTTGGTCTCACGCTGAGTCTGCTGATCACCCA 290
Qy	276	CGTCGTCCTCATCGTCGCGGTTCTGCTGCCGGTCGGGTGTAGCTCTGCCACCATCCCCG 335
Db	291	ACAAGACCTAGCTCCCCAGCAGAGATGGCCCCACAACAAAAGAGGTCCAGGCCCTCAGA 350
Qy	336	GCAGGACGAAGTCCCCAGCAGACAGTGGCCCCACAGCACAGAGGCGCAGCTCAAGGA 395
Db	351	GGGATTGTGTCACCTGGACACCATACTCAGAAGACGGTAGAGATTGCACTCCTGCAA 410
Qy	396	GGAGGAGTGTCCACCGAGGATCTCATAGATCAGAATACTGGACCTGTAACCCGTGCAC 455
Db	411	ATATGGACAGGACTATAGCACTACTGGATGACCTCCTTTCTGCTTGCCTGCACCAAG 470
Qy	456	AGAGGGTGTGGATTACACCATTTGCTTCAACAAATTGGCTTCTGCTGCTATGTACAGT 515
Db	471	GTGTGATTCAAGGTGAACTGGAGCTAACGTCCTGCACCCACGACAGAGAACACAGTGTGTCA 530
Qy	516	TTGTAAATCAGGTCAAACAAATAAAAGTCTCTGTACACGACGACAGACACCCGTGTCA 575
Db	531	GTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCTGAGATGTGCCGGAAAGTGCCGCAC 590
Qy	576	GTGTGAAAAAGGAAGCTCCAGGATAAAACTCCCTGAGATGTGCCGGACGTGTAGAAC 635
Db	591	AGGGTGTCCAGGGATGGTCAAGGTGTGAGTGTACACCTGGAGTGCACATCGAATC 650

Qy	636	AGGGTGTCCCCAGAGGGATGGTCAGGTCAGTAATTGTACGGCCCGGAGTGACAT-AA-G	693
Db	651	TGTCCACAAAAGAATCAGGTACAAGCACAGTGGGGAAAGCCCCAGCTGTGGAGGAGACGGT	710
Qy	694	TG-CAAAAATGAATCAGCTGCCAGTTCACTGGAAAACCCCAGCACGGAGGAGACAGT	752
Db	711	GACCTCCAGGCCAGGGACTCTGCCCTCCCTGTT-CTCTCTCAGG--CATCATCATAGG	767
Qy	753	GACCACCATCTGGGATGCTGCCCTCCCTATCACTACCTTATCATCATAGTGGTTT	812
Db	768	AGTCACAGTTGCAGCGTAGTCTGTGGCTGTGTT-GTTTCAAGTCTTACTGT	826
Qy	813	AGTCATCATTTAGCTGTGGTTGCTGCTTTCATGTCGAGAAAATCATTTCTTA	872
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Qy	873	CCTCAAAGGCATCTGCTCAGGGTGGAGGAGGTCCCGAACGTGTCACAGAGTCCTTT	932
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Qy	933	CCGGCGGCGTTCATGTCCTCACGAGTCTGGGGCGAGGACAATGCCCGAACGAGAC	992
Db	942	CGTGAGTA-----T-CTTGCAGCCCCACCCAGGTCTCTGAGCAGGAATGGAAAGTCAGGA	995
Qy	993	CCTGAGTAACAGATACTTGCAGCCCCACCCAGGTCTCTGAGCAGGAATCCAAGGTCAAGGA	1052
Db	996	GCCACGAGGCCAACAGGTGTCACACATGTGTCCCCCGGGAGTCAGAACATCTCTGGA	1055
Qy	1053	GCTGGCAGAGTAACAGGTGTGACTCTAGACTYGCAGAGGAGGCCAACAGGTCTGCTGGA	1112
Db	1056	ACCGGCAGAGCTGAAAGGTCTCAGAGGGAGGCTGCTGGTCCACCAAATGAAGGTGA	1115
Qy	1113	ACAGGCAGAGCTGAGGGTGTAGAGGAGGAGGTGCTGGTCCAGTGAATGACGCTGA	1172
Db	1116	TCCCACGTGA 1124	
Qy	1173	CTCCGCTGA 1181	

**RESULT** 10  
**LOCUS** AF016849 1859 bp mRNA PRI 07-OCT-1997  
**DEFINITION** Homo sapiens apoptosis inducing receptor TRAIL-R2 (TRAILR2) mRNA, complete cds.  
**ACCESSION** AF016849  
**NID** g2465585  
**KEYWORDS**  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 1859)  
**AUTHORS** Walczak,H., Degli-Esposti,M.A., Johnson,R.S., Smolak,P.J.,  
Waugh,J.Y., Boiani,M., Timour,M.S., Gerhart,M.J., Schooley,K.A.,  
Smith,C.A., Goodwin,R.G. and Rauch,C.T.  
**TITLE** TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL  
**JOURNAL** EMBO J. 16 (17), 5386-5397 (1997)  
**MEDLINE** 97459925  
**REFERENCE** 2 (bases 1 to 1859)  
**AUTHORS** Walczak,H.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (31-JUL-1997) Immunobiology, Immunex Corp., 51 University  
St., Seattle, WA 98101, USA  
**FEATURES** Location/Qualifiers  
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**gene** 1. 1859  
/gene="TRAILR2"  
**CDS** 145..1467

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apoptosis-mediating receptor for TRAIL"
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/db_xref="PID:g2465586"
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PRGMVKVGDTWSDIECVHKESGTKHSGEAPAVEETVTSSPPTPASPCLSGLIIVG
TVAAVLIVAVFVCKSLIWKVLPYKICGCGGGDPVERDRSQRPGAEQDNVLNETV
SILQPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLLEPAEERQSRRLLV PANEGDP
TETLRQCFFDDFDADLVPFDSEPLMRKLGMDNEIKVAKAAGHRDTLYTMLIKWVNK
TCRDASVHTLDAEFTLGERLAKQKIEDHLLSGKPMYLEGNADSAMS"

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BASE COUNT 458 a 471 c 511 g 419 t  
 ORIGIN

Query Match 12.4%; Score 259; DB 28; Length 1859;  
 Best Local Similarity 68.3%; Pred. No. 1.0e-195;  
 Matches 703; Conservative 1; Mismatches 301; Indels 24; Gaps 17;

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Db 144 CATGGAACAACGGGGACAGAACGCCCGGCCCTCGGGGGCCCGAAAAGGCACGGCCC 203
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT	11	LOCUS	HSU90875	1407 bp	mRNA	PRI	19-APR-1997
DEFINITION	Human cytotoxic ligand TRAIL receptor mRNA, complete cds.						
ACCESSION	U90875						
NID	g1945071						
KEYWORDS	.						
SOURCE	human.						
ORGANISM	Homo sapiens						
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE	1 (bases 1 to 1407)						
AUTHORS	Pan,G., O'Rourke,K., Chinnaiyan,A.M., Gentz,R., Ebner,R., Ni,J. and Dixit,V.M.						
TITLE	The receptor for the cytotoxic ligand TRAIL						
JOURNAL	Science 276 (5309), 111-113 (1997)						
MEDLINE	97238921						
REFERENCE	2 (bases 1 to 1407)						
AUTHORS	Pan,G., O'Rourke,K., Chinnaiyan,A.M., Gentz,R., Ebner,R., Ni,J. and Dixit,V.M.						
TITLE	Direct Submission						
JOURNAL	Submitted (25-FEB-1997) Pathology, University of Michigan, 1301 Catherine Road, Ann Arbor, MI 48109, USA						
FEATURES	Location/Qualifiers						
source	1..1407						
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CDS	1..1407						
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	/codon_start=1						
	/product="cytotoxic ligand TRAIL receptor"						
	/db_xref="PID:g1945072"						
	/translation="MAPPPARVHGLAFAVTPNPGSAASGTEAAAATPSKVGWSAGRIPRGGRRGALPTSMQHGPSARARAGRPRPARAPSPRLRVHKTFKVVVGVLQVVPSSAATIHLHQSTIQQWEHSPLGECPGSHSERPGACNRCTEGVYTNASNLLFACLPCTACKSDEEEERPCTTRNTACQCKPGTFRNDNSAEMCRKCTGCPGRMVKNLFDCPWSDIECVHKESGNHNIWVILVTVPLVLLAVLIVCCIGSCGGDPKCMDRVCFWRLQLRGPAEADNAHNEILSNADSLSTFVSEQCMESQEPADLITGTVQSPGEAQCLLGPAEAGSQRRLLVPANGADPTETLMFFDKFANIVPFDSDWDQLMRQLDLTKNEIDVVRAGTAGPGLDALYAMLWVNKTGRNASIHTLDALEMERHAKEKIQDLDVSKGFIYLEDGTGSAVSLE"						
BASE COUNT	328 a 355 c 434 g 290 t						
ORIGIN							
Query Match	9.7%	Score 202; DB 28; Length 1407;					
Best Local Similarity	78.7%	Pred. No. 1.06e-144;					
Matches	277	Conservative 0; Mismatches 75; Indels 0; Gaps 0;					
Db	335 AACTCATGATCAATCAATTGGCACACAGCAATGGGAACATAGCCCTTGGGAGAGTT	394					
Qy	344 AAGTCCCCAGCAGACTGGCCACAGCAACAGAGCAGCTGGCAGGAGGAGGT	403					

Db 395 GTCCACCAGGATCTCATAGATCAGAACGTCTGGACCGTAAACCGGTGACAGAGGTG 454  
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 Qy 404 GTCCACCAGGATCTCATAGATCAGAACGTCTGGACCGTAAACCGGTGACAGAGGTG 463  
 Db 455 TGGTTTACACCAATGCTTCAAACAAATTGTTGCTTCATGTCAGCTTGAAAT 514  
       ||||||| ||||| ||||| ||||| ||||| |||||  
 Qy 464 TGGATTACACCATTGCTTCAAACAAATTGCTCTGCTGCTGCTATGTCAGCTTGAAAT 523  
 Db 515 CAGATGAAGAAGAGAGACTCCCTGCCAACGACAGAACACACCATGTCAGTCAAAC 574  
       ||||||| ||||| ||||| ||||| ||||| |||||  
 Qy 524 CAGGTCAAACAAATAAAAGTCTTGTACACGACAGAACACCGTGTGTCAGTGTAAA 583  
 Db 575 CAGGAACCTTCCGAATGACAATTGCTGAGATGTGCCGAAGTGCAGCACAGGGTGC 634  
       ||||||| ||||| ||||| ||||| ||||| |||||  
 Qy 584 AAGGAAGCTTCCAGGATAAAACTCCCTGAGATGTGCCGAAGTGTAGAACAGGGTGT 643  
 Db 635 CCAGAGGGATGGTCAAGGTCAAGGATTGACGCCCTGGACTGACATCGAGT 686  
       ||||||| ||||| ||||| ||||| |||||  
 Qy 644 CCAGAGGGATGGTCAAGGTCAATTGTACGCCCGAGTGCACATCAAGTG 695

RESULT 12  
 LOCUS AF020501 1236 bp mRNA PRI 28-SEP-1997  
 DEFINITION Homo sapiens cytotoxic TRAIL receptor-2 (DR5) mRNA, complete cds.  
 ACCESSION AF020501  
 NID g2443817  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1236)  
 AUTHORS MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T.,  
 Cohen,G.M. and Alnemri,E.S.  
 TITLE Identification and Molecular Cloning of Two Novel Receptors for the  
 Cytotoxic ligand TRAIL  
 JOURNAL J. Biol. Chem. (1997) In press  
 REFERENCE 2 (bases 1 to 1236)  
 AUTHORS MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T.,  
 Cohen,G.M. and Alnemri,E.S.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-AUG-1997) Department of Microbiology and Immunology,  
 Kimmel Cancer Institute, 233 S. 10th Street, Philadelphia, PA  
 19107, USA

FEATURES Location/Qualifiers  
 source 1. .1236  
       /organism="Homo sapiens"  
       /db\_xref="taxon:9606"  
       /cell\_type="T-lymphocyte"  
       /note="Jurkat"  
 gene 1. .1236  
       /gene="DR5"  
 CDS 1. .1236  
       /gene="DR5"  
       /note="TNFR family member; binds cytotoxic ligand TRAIL"  
       /codon\_start=1  
       /product="cytotoxic TRAIL receptor-2"  
       /db\_xref="ID:g2443818"  
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 PRGMVKVGDCTPWSDEICVHKESGIIGVTVAAVVLLIVAVFCKSLLKKVLYLKGI  
 CGGGGGDPERVDRSSQRQGAEDNVLNIEVISILOPTQVPEQEMEVQEPAEPTGVNMLSP  
 GESEHLLPEAERSQRRLLVPALEGDPTEILRCFDDFADLVPFDSWEPLMRKLGL  
 MDNEIKVAKAEAAGHRDTLYTMLIKWVNKTGRDASVHTLLDAETLGERLAKQKIEDH  
 LLSGGKFMYLEGNAUDSAM"

BASE COUNT 302 a 314 c 372 g 248 t  
 ORIGIN

Query Match 9.4%; Score 195; DB 28; Length 1236;  
 Best Local Similarity 70.9%; Pred. No. 1.75e-138;

Matches 382; Conservative 0; Mismatches 151; Indels 6; Gaps 4;  
 Db 1 ATGGAACACGGGGACAGAACGCCCGGCTCGGGGGCCCGAAAAGGCACGGCCA 60  
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 Qy 157 ATGGGACTTGGGACAAGCGTCCCGACCGCCTGAGCGCTCGACCGCGCTATCCA 216  
 Db 61 GGACCCAGGGAGGCCGGAGCCAGGCCCTGGCTCCGGTCCCCAAGACCCCTT-GTGC 118  
       ||||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Qy 217 GGACCCAGGACAGCGTGGGAACAGACCATGGCTCTGGACCCCAGATCCTTAAGTC 276  
 Db 119 -TCGT--TG-TGCGCGGCTCTGCTGTTGGTCTCAGCTGAGTCTGCTGATCACCAA 174  
       ||||||| ||||| ||||| ||||| ||||| |||||  
 Qy 277 GTCGCTTCATCGTCGGGTTCTGCTGCCGGTCCGGTTGACTCTGCCACCATCCCCCG 336  
 Db 175 CAAGACCTAGCTCCCGACAGAGACTGGCCCAACAAACAAAAGGGTCAGCCCCCTCAGAG 234  
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 Qy 337 CAGGACGAAGTCCCCAGCAGACAGTGGCCCCACAGCAACAGAGGCCAGCCTCAAGGAG 396  
 Db 235 GGATTGTGTCACCTGGACACCATATCTCAGAAGACGGTAGAGATGCTATCTCTGCAA 294  
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 Qy 397 GAGGAGTGTCCAGCAGGATCTCATAGATCAGAAATATACGGACCTGTAACCCGTGACA 456  
 Db 295 TATGGACAGGACTATAGCACTACTGGAATGACCTCTTTCTGCTTGCCTGCACCAAGG 354  
       ||||||| |||||  
 Qy 457 GAGGGGTGTTGATTACACCATGCTTCAACAAATTGCTTCTTGCTGCTATGTACAGTT 516  
 Db 355 TGTGATTCAAGGTGAAGTGGAGCTAAGTCCCTGACACGACAGAAACACAGTGTGCAG 414  
       ||||||| |||||  
 Qy 517 TGTAAATCAAGTCAAACAAATAAAAGTCTCTGACACGACAGACACCCGTGTGCAG 576  
 Db 415 TGCGAAGAAGGCACCTTCCGGAGAAGATTCTCTGAGATGTGCCGAAGTGGCGCACA 474  
       ||||||| |||||  
 Qy 577 TGTAAAAAGAAGCTTCCAGGATAAAACTCCCTGAGATGTGCCGAAGTGTAGAACAA 636  
 Db 475 GGGTGTCCCAGAGGGATGGTCAAGGTGGTGATTGATCACCCCTGGAGTGCACATCGAATG 533  
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 Qy 637 GGGTGTCCCAGAGGGATGGTCAAGGTCAAGTAATGATCACCCGGAGTGCACATCAAGTG 695

RESULT 13  
 LOCUS AF018657 1236 bp mRNA PRI 18-SEP-1997  
 DEFINITION Homo sapiens apoptosis inducing protein (TRICK2A) mRNA, complete cds.  
 ACCESSION AF018657  
 NID g2407650  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1236)  
 AUTHORS Scream,G.R., Mongkolsapaya,J., Xu,X., Cowper,A.E., McMichael,A.J.  
 and Bell,A.J.  
 TITLE TRICK2 a new alternatively spliced receptor which transduces the  
 cytotoxic signal from TRAIL  
 JOURNAL Curr. Biol. (1997) In press  
 REFERENCE 2 (bases 1 to 1236)  
 AUTHORS Scream,G.R., Mongkolsapaya,J., Xu,X., Cowper,A.E., McMichael,A.J.  
 and Bell,A.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-AUG-1997) Molecular Immunology, Institute of  
 Molecular Medicine, Oxford University, John Radcliffe Hospital,  
 Headington, Oxford OX3 9DS, UK  
 FEATURES Location/Qualifiers  
 source 1. .1236  
       /organism="Homo sapiens"  
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 CDS 1. .1236  
       /gene="TRICK2A"  
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contains 2 TNF-R repeats and cytoplasmic death domain"  
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 /db\_xref="PID:g2407651"  
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 PRGMVKVGDCTPWSIECVHKESGIIIVGTVAAVVLIVAVFVCKSLWKKVLPYLKG  
 CSGGGDPERVDRSSQRPGAEVNVLNEIVSILQPTQVPEQEVQEPAPGVNMMLSP  
 GESEHLLPEAERSORRRLV PANEGDPTETLRCQCFDDFADLVPFDWEPLMRKLG  
 MDNEIKVAKAEAAGHRDTLYTMLIKWNKTGRDASVHTLDAETLGERLAKQKIEDH  
 LLSSGKFMYLEGNADSMS"

BASE COUNT 302 a 314 c 372 g 248 t  
 ORIGIN

Query Match 9.4%; Score 195; DB 28; Length 1236;  
 Best Local Similarity 70.9%; Pred. No. 1.75e-138;  
 Matches 382; Conservative 0; Mismatches 151; Indels 6; Gaps 4;

Db 1 ATGGAACACAACGGGGACAGAACGCCCGCCGCTCGGGGGCCGGAAAAGGCACGGCCA 60

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 157 ATGGGACTTTGGGGACAACGGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGTATCCA 216

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Db 61 GGACCCCAGGGAGGGCCGGGAGCCAGGCCCTGGGCTCCGGTCCCCAGACCCCTT-GTGC 118

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Qy 217 GGAGGCCAGGACAGCCTCGGGACCAGACCATGGCTCTGGACCCCAAGATCCTTAAGTC 276

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Db 119 -TCGT--TG-TGCCCGCGTCCTGCTGTTGAGCTGAGTCGCTGATCACCCAA 174

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Qy 277 GTCTCTTCATCGTCGCCGTTCTGCTGCCGGTGTGACTCTGCCACCATCCCCGG 336

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Db 175 CAAGACCTAGCTCCCCAGCAGAGACTGGCCCCAACACAAAGAGGTCCAGCCCTCAGAG 234

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Qy 337 CAGGACGAAGTTCCCCAGCAGACAGTGGCCCCAACAGAACAGGGCCAGCCTAACGGAG 396

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Db 235 GGATTGTGTCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGACATCTCGCAA 294

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 397 GAGGAGTGTCCAGCAGGATTCATAGATCAGAAATACTGGAGCTGTAAACCGTGCACA 456

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Db 295 TATGGACAGGACTATAGCACTACTGGAAATGACCTCCCTTCTGCGCTGCACCAAG 354

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Qy 457 GAGGGTGTGGATTACACCATTGCTTCAACAAATTGCTCTTGCCTGCTATGTACAGTT 516

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Db 355 TGTGATTTCAGGTGAAGTGGAGCTAAGTCCCTGACCCACGACAGAAACACAGTGTGTCAG 414

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Qy 517 TGTAAATCAGGTCAAACAAATAAAGTTCTGTACACGACCAAGACACCGTGTGTCAG 576

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Db 415 TCCGAAGAAGGCACCTCCGGAAAGAAGATTCTCTGAGATGTGCCGGAAAGTCCGCA 474

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Db 475 GGGTGTCCCAGAGGGATGGTCAAGGTCGGTATTGTAACCCCTGGAGTGACATCGAATG 533

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Qy 637 GGGTGTCCCAGAGGGATGGTCAAGGTCAGTAATTGTAACGCCCGGAGTGACATCAAGTG 695

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RESULT 14  
 LOCUS AF016268 1717 bp mRNA PRI 05-FEB-1998

DEFINITION Homo sapiens death receptor 5 (DR5) mRNA, complete cds.

ACCESSION AF016268

NID g2832229

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1717)  
 AUTHORS Chaudhary, P.M., Eby, M., Jasmin, A., Bookwalter, A., Murray, J. and Hood, L.

TITLE Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway

JOURNAL Immunity 7 (6), 821-830 (1997)

MEDLINE 98090092  
 REFERENCE 2 (bases 1 to 1717)  
 AUTHORS Chaudhary, P.M., Eby, M., Jasmin, A., Bookwalter, A. and Hood, L.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUL-1997) Molecular Biotechnology, University of Washington, NE Pacific Street, Box 357730, Seattle, WA 98195-7730, USA  
 FEATURES Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 gene 1..1717  
 /gene="DR5"  
 CDS 110..1345  
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 /function="induces FADD dependent apoptosis and activates NF-kappa B pathway"  
 /note="similar to TRAIL receptor (DR4)"  
 /codon\_start=1  
 /product="death receptor 5"  
 /db\_xref="PID:g2832230"  
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 PRGMVKVGDCTPWSIECVHKESGIIIGTVAAVVLIVAVFVCKSLWKKVLPYLKG  
 CSGGGDPERVDRSSQRPGAEVNVLNEIVSILOPTVPEQEMEVQEPAPGVNMMLSP  
 GESEHLLPEAERSORRRLV PANEGDPTETLRCQCFDDFADLVPFDWEPLMRKLG  
 MDNEIKVAKAEAAGHRDTLYTMLIKWNKTGRDASVHTLDAETLGERLAKQKIEDH  
 LLSSGKFMYLEGNADSMS"

BASE COUNT 437 a 425 c 467 g 388 t  
 ORIGIN

Query Match 9.4%; Score 196; DB 28; Length 1717;  
 Best Local Similarity 70.9%; Pred. No. 2.27e-139;  
 Matches 383; Conservative 0; Mismatches 151; Indels 6; Gaps 4;

Db 109 CATGGAACACAACGGGGACAGAACGCCCGCCGCTCGGGGGCCGGAAAAGGCACGGCC 168

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 156 CATGGGACTTTGGGACAACAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCC 215

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Db 169 AGGACCCAGGGAGGCGCGGGAGGCCAGGCGCTGGCTCGGGTCCCCAAGACCCCTT-GTGC 226

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 216 AGGAGCCAGGACAGCGTCCGGAAACAGACCATGGCTCTGGACCCCAAGATCCTTAAGT 275

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 227 C-TCGT--TG-TCGCGCGGTCTGCTGTTGAGCTAGCTGAGTCTGCTCTGATCACCC 282

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 276 CGTCGCTCTTCATCGTCGGGTTCTGCTGCCGGTCCGGGTGACTCTCCACCATCCCC 335

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 283 ACAAGACCTAGCTCCCCAGCAGAGACTGGCCCAACAAAGAGGTCCAGCCCTCAGA 342

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 336 GCAGGACGAAGTTCCCAGCAGACAGTGGCCCAACAGCAACAGGGCGCAGCTCAAGGA 395

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 343 GGGATTGTGTCACCTGGACCCATATCTCAGAACAGGTAGAGATTGACATCTCTGCAA 402

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 396 GGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAATACTGGAGCTGTAACCCGTGAC 455

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 403 ATATGGACAGGACTATAGCACTACTGGAAATGACCTCTTCTGCTGCGCTGCACCA 462

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 456 AGAGGGTGTGGATTACACCATGTCCTCAACATTTGCTCTTGTCTGCTATGTCAGT 515

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 463 GTGTGATTCAAGGTGAAGTGGAGCTAAGTCCCTGACCCAGACGAGAAACACAGTGTCA 522

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 516 TTGTAATCAGGTCAAACAAATAAAAGTTCTGTACACGACCAAGAGACACCGTGTCA 575

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 523 GTGCCAAGAAGGCACCTTCCGGAAAGAAGATTCTCTGAGATGTGCCGGAGTCCGCAC 582

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 576 GTGTGAAAAGGAAGCTTCCAGGATAAAACTCCCTGAGATGTGCCGGAGTGTAGAAC 635

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 583 AGGGGTGTCCCAGAGGGATGGTCAAGGTGGTGTACACCTGGAGTGACATCGAATG 642

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 636 AGGGGTGTCCCAGAGGGATGGTCAAGGTCAAGGTCAAGTAAATTGTAACGCCGGAGTCAACTG 695

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

**RESULT** 15  
**LOCUS** AF012535 1799 bp mRNA PRI 21-AUG-1997  
**DEFINITION** Homo sapiens death receptor 5 (DR5) mRNA, complete cds.  
**ACCESSION** AF012535  
**NID** g2338419  
**KEYWORDS**  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
Homo.  
**REFERENCE** 1 (bases 1 to 1799)  
**AUTHORS** Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Skubatch,M.,  
Baldwin,D., Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I.,  
Goddard,A.D., Godowski,P. and Ashkenazi,A.  
**TITLE** Control of TRAIL-induced apoptosis by a family of signaling and  
decoy receptors  
**JOURNAL** Science 277 (5327), 818-821 (1997)  
**MEDLINE** 97390509  
**REFERENCE** 2 (bases 1 to 1799)  
**AUTHORS** Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Baldwin,D.,  
Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I., Goddard,A.D.,  
Godowski,P. and Ashkenazi,A.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (06-JUL-1997) Molecular Oncology, Genentech, 1 DNA Way,  
South San Francisco, CA 94080, USA  
**FEATURES**  
**source** Location/Qualifiers  
1..1799  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
**gene** 1..1799  
/gene="DR5"  
**CDS** 140..1375  
/gene="DR5"  
/note="tumor necrosis factor receptor family member;  
mediates apoptosis induction by TRAIL/Apo2L."  
/codon\_start-1  
/product="death receptor 5"  
/db\_xref="PID:g2338419"  
/translation="MEQORGONAPAASCARKRHGPGPREARGARGLRVPKTLVVA  
VLLLSAESAELITQDIAQPQQRAAPQQKRSSPSEGLCPPGHHSIEDGRDCISCKYQGD  
YSTHWNDLLFCRLRCRDGSVEVLSPCTTNTVCQCEEGTFREEDSPCMRKCRTGC  
PRGVVKVGCTCPWSDIECIVKESGIIGVTVAAVVLIVAFVCKSSLWKKVLPYLG  
CSGGGGDPERVDRSSORGAEDNVNLNEIVSILQOPTQVPEQEMEVQEPAEPTGVNMLSP  
GESEHLLPEAERSQRRLLVPAANEQDPTEITLRQCFDDPAIDLVPFDWSPELMRKLGL  
MDNEIKVAKAAEAGHRDTLYTMLIKWVNKTGRDAVSHLLDAETLGERLAKQKIEDH  
LLSSGKEMYLEGNADSLA"  
  
**BASE COUNT** 459 a 454 c 490 g 396 t

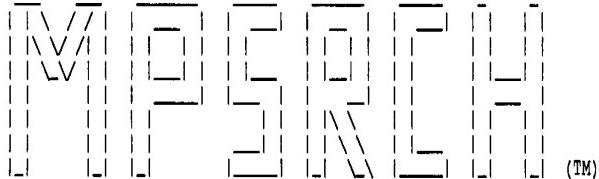
BASE COUNT 459 a 454 c 490 g 396 t  
ORIGIN

Query Match 9.3%; Score 194; DB 28; Length 1799;  
Best Local Similarity 70.7%; Pred. No. 1.35e-137;  
Matches 382; Conservative 0; Mismatches 152; Indels 6; Gaps 4;

Db	139	CATGGAAACACGGGGACAGAACGCCCGGCGCTCGGGGGCCCGAAAAGGCACGGCC 198
Qy	156	CATGGGACTTGGGACAAAGCGTCCCACGCCCTCGAGGCCCTCGAGCAGGGCCTATCC 215
Db	199	AGGACCCAGGGAGGCCCCGGGAGCCAGGCCCTGGCTCCGGTCCCCAAGACCCCT--GTG 256
Qy	216	AGGAGCCAGGGACAGCGTCGGGAACAGACCATGGCTCTGGACCCCCAAGATCTTAAGGT 275
Db	257	C-TCGT--TG-TCCGGCGGTCTGCTGTTGGTCTCACCTGAGTCGCTCTGATCACCCA 312
Qy	276	CGTCGCTTCATCGTCGCGGTTCTGCTGCCGGTCCGGTTGACTCTGCCACCATCCCCG 335
Db	313	ACAAGACCTAGCTCCCCAGCAGAGGGGCCCAACAACAAAAGAGGTCCAGGCCCTCAGA 372
Qy	336	GCAGGACGAAGTCCCCAGCAGACAGTGGCCCCACAGCAACAGAGGGCGCAGCTCAAGGA 395
Db	373	GGGATTGTGTCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCTGCAA 432

Search completed: Fri May 15 18:23:10 1998  
Job time : 2268 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 14 16:48:14 1998; MasPar time 19.72 Seconds  
824.206 Million cell updates/sec

Tabular output not generated.

Title: >US-08-918-874-1  
Description: (1-386) from US08918874.pep  
Perfect Score: 2715  
Sequence: 1 MGLWQGSVPTASSARAGRYP.....VGSEKLFYEEDEAGSATSC 386

Scoring table: PAM 150  
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: sptrmbl15  
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal  
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant  
9:sp\_bacteria 10:sp\_rat 11:sp\_virus 12:sp\_vertebrate  
13:sp\_unclassified

Statistics: Mean 47.012; Variance 94.359; scale 0.498

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	%	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1060	39.0	440	2	015531	APOPTOSIS INDUCING PRO	1.72e-185			
2	1044	38.5	440	2	014763	APOPTOSIS INDUCING REC	3.54e-182			
3	834	30.7	299	2	014798	CYTOTOXIC TRAIL RECEPT	6.40e-139			
4	820	30.2	259	2	014755	TRAIL RECEPTOR 3.	4.69e-136			
5	811	29.9	411	2	015517	CYTOTOXIC TRAIL RECEPT	3.25e-134			
6	804	29.6	411	2	014720	DEATH RECEPTOR 5.	8.74e-133			
7	795	29.3	411	2	015508	P53-REGULATED DNA DAMA	6.02e-131			
8	784	28.9	468	2	000220	CYTOTOXIC LIGAND TRAIL	1.06e-128			
9	192	7.1	471	4	019131	TUMOR NECROSIS FACTOR-	3.21e-14			
10	191	7.0	459	10	Q62327	TUMOR NECROSIS FACTOR	4.71e-14			
11	187	6.9	348	11	Q85407	HOMOLOG OF VACCINIA VI	2.16e-13			
12	187	6.9	349	11	Q89098	GARCIA-1966 RIGHT NEAR	2.16e-13			
13	187	6.9	349	11	Q89118	SOMALIA-1977 RIGHT NEA	2.16e-13			
14	186	6.9	355	11	Q85308	SECRETED RECEPTOR BIND	3.16e-13			
15	182	6.7	314	2	Q14293	FAS SOLUBLE PROTEIN.	1.44e-12			
16	176	6.5	324	10	Q63199	FAS ANTIGEN PRECURSOR.	1.36e-11			
17	176	6.5	401	10	008727	OSTEOPROTEGERIN.	1.36e-11			
18	175	6.4	401	10	008712	OSTEOPROTEGERIN.	1.97e-11			
19	167	6.2	401	2	000300	OSTEOPROTEGERIN.	3.78e-10			
20	157	5.8	283	2	Q92956	HERPESVIRUS ENTRY MEDI	1.41e-08			

21	158	5.8	425	2	Q16042	TUMOR NECROSIS FACTOR	9.87e-09
22	151	5.6	180	4	Q95185	TUMOUR NECROSIS FACTOR	1.19e-07
23	130	4.8	274	2	Q13663	CELL SURFACE ANTIGEN O	1.55e-04
24	128	4.7	267	4	Q02764	OX40 PRECURSOR (FRAGME	2.99e-04
25	127	4.7	493	10	P97525	CD30 PRECURSOR.	4.14e-04
26	122	4.5	498	10	Q60846	CD30 ANTIGEN.	2.07e-03
27	117	4.3	176	11	Q68396	ORF UL144.	1.00e-02
28	111	4.1	183	11	Q65272	J13L GENE (ISOLATE LIS	6.32e-02
29	111	4.1	183	11	Q65194	STRUCTURAL PROTEIN P54	6.32e-02
30	111	4.1	185	11	Q65271	J13L GENE (ISOLATE LIS	6.32e-02
31	110	4.1	512	9	Q47631	SEPC.	8.54e-02
32	110	4.1	1357	3	Q22453	SIMILARITY LDL RECEPTOR	8.54e-02
33	108	4.0	85	10	Q63352	MYOSIN HEAVY CHAIN (FR	1.55e-01
34	109	4.0	176	11	Q89784	POTENTIAL SIGNAL PEPTI	1.15e-01
35	109	4.0	189	11	Q65273	J13L GENE (ISOLATE RSA	1.15e-01
36	109	4.0	191	11	Q65274	J13L GENE (ISOLATE TAN	1.15e-01
37	105	3.9	189	11	Q65270	J13L GENE (ISOLATE LIL	3.75e-01
38	107	3.9	1372	3	P91526	SIMILARITY TO MULTIPLE	2.08e-01
39	105	3.9	2621	3	P90891	P55H12.3.	3.75e-01
40	102	3.8	431	9	Q52146	HYPOTHETICAL 43.7 KD P	8.89e-01
41	103	3.8	506	3	Q17598	C03A3.2.	6.68e-01
42	102	3.8	988	12	Q07498	TYROSINE KINASE CEK10	8.89e-01
43	104	3.8	1931	12	Q91973	SLOW MYOSIN HEAVY CHAI	5.01e-01
44	101	3.7	196	11	Q65275	J13L GENE (ISOLATE UGA	1.18e+00
45	101	3.7	1939	2	Q13943	CARDIAC ALPHA-MYOSIN H	1.18e+00

#### ALIGNMENTS

RESULT	1	ID	015531	PRELIMINARY;	PRT;	440 AA.
AC	015531;					
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	APOPTOSIS INDUCING PROTEIN.					
GN	TRICK2B.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; PRIMATES.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	SCREATION G.R., MONGKOLSAPAYA J., XU X., COWPER A.E., MCMICHAEL A.J.,					
RA	BELL A.J.;					
RL	CURR. BIOL. 0:0-0(1997).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RA	SCHNEIDER P., BODMER J.-L., THOME M., HOLLER N., HOFMANN K.,					
RA	TSCHOPP J.;					
RL	FEBS LETT. 0:0-0(1997).					
DR	EMBL; AF018658; G2407653; -.					
DR	EMBL; AF016266; G2529563; -.					
SQ	SEQUENCE 440 AA; 47894 MW; 8DD4EF03 CRC32;					
Query Match 39.0%; Score 1060; DB 2; Length 440;						
Best Local Similarity 53.7%; Pred. No. 1.72e-185;						
Matches 187; Conservative 50; Mismatches 93; Indels 18; Gaps 8;						
Db	1 MEQRGQNAPAASGARKRHPGPAREARGPGLRPKTLVLVV--AVAVLLVSAESALITQ 58					
Qy	:   :  :   :   :   :   :   :   :   :   :   :   :   :   :   :					
Qy	1 MGLWQGSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVPIAVVLPVRVDSATIPR 60					
Db	59 QDLAPQQRVAPQQKRSSPSEGCPGHHISEDGRDCISCKYQGDYSTHWNDLLFCRLCTR 118					
Qy	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
Qy	61 QDEVPPQQTVAPQQQRSLKEEECPAGSHRSEYTGCNPCTEGVDYTIASNNLPSCLLCV 120					
Db	119 CDSGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCRKRTGCPGRMVKGVDCTPWSDIEC 178					
Qy	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
Qy	121 CKSGQTNKSSCTTTRDTCQCCEKGSFQDKNSPEMCRTCRTGCPGRMVGVNSCTPRSDIRC 180					
Db	179 VHKESGTKHSGEAPAVEETVTSSPCTPASPSCSLSGIIIGVTVAAVVLLIVAFVCKSLWLK 238					
	:   :  :  :   :   :  :   :   :   :   :   :   :   :   :   :   :					

Qy	181	-KNESAASSTGKTPAAEVTVTILGMLASPYHIL-IIIVLVIIAVVVVGFSR---K	234
D <sub>b</sub>	239	KVLPYLGICSGGGDPERVDR-----SSQ-R-PGAEDNVLNEIVSI--LQPTQVPEQE	288
		:   :   :   :	
Qy	235	KFTISYLKGICSGGGGPERVHVRVLRRRSCPSRVPGAEQNARNETLSNRVILQPTQVSEQE	294
D <sub>b</sub>	289	MEVQEPAPTEPTGVNMLSPGESEHLLPEAEAERSQRRLLV PANEGDPTE	336
		:           :     :	
Qy	295	IQQQELAELTGTVEXPPEPQRLLEQAEAEGCQRRRLVPVN DADSAD	342

RESULT 2  
ID 014763 PRELIMINARY; PRT; 440 AA.

AC 014763;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE APOPTOSIS INDUCING RECEPTOR TRAIL-R2.  
GN TRAILR2.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA WALCZAK H., DEGLI-ESPOSTI M.A., JOHNSON R.S., SMOLAK P.J., WAU  
RA BOIANI M., TIMOUR M.S., GERHART M.J., SCHOOLEY K.A., SMITH C.A.  
RA GOODWIN R.G., RAUCH C.T.;  
RL EMBO J. 16:5386-5397(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA WALCZAK H.;  
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDJB DATA BANKS.  
DR EMBL; AF016849; G2465506; -.  
SQ SEQUENCE 440 AA: 47850 MW: 268DA232 CRC32:

Query Match 38.5%; Score 1044; DB 2; Length 440;  
Best Local Similarity 52.7%; Pred. No. 3.54e-182;  
Matches 184; Conservative 54; Mismatches 91; Indels 20; Gaps 9;

Db	1	MEQRQNPAAASGARKRHPGPVREARGARP--GPRVPKTLVLVVAANLLVSAESALIT 57
:  :		
Qy	1	MCLWQSVPASSARAGRYPGARTASGTRPWLDPKILKFVVFTVA-VLPPVRVDSATIP 59
:  :		
Db	58	QDQLAPQQRRAFPQQKRSSPSSEGLCPPGHHISEDCRDICISKYQDYSTHWNDLFLCRLCT 11
:  :		
Qy	60	RQDEVPPQTVAPQQQRSLEEECPAGSHRSEYTGCACNPCTEGVDYTIASNLLPSCLLCT 11
:  :		
Db	118	RCDSGEVELSPCTTRNTVCQCEGTFREEDSPEMCRKRTGCPGRMVKGDCPTWSDIE 17
:  :		
Qy	120	VCKSGQTNKSSCTTRDTVCQCEKGFSQFDKNSPEMCRKRTGCPGRMVKGVSNCPTRSIDK 17
:  :		
Db	178	CVKHESGTKHSGEPAVEETVTSSPGTPASPCSLSGIIGVTAAVVLIVAVFVKCSLLW 23
:  :		
Qy	180	C-KNESAASTGKTPAABETVTILGMLASPYHIL-IIIWLVIIIAVAVVVGFSCR---- 23
:  :		
Db	238	KKVLPYLKGICSGGGDPERVDR-----SSQ-R-PGAEDNVLEIVSI---LQPTQVPEQ 28
:  :		
Qy	234	KKFISYLKGICSGGGGPERVHRLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQ 29
:  :		
Db	288	EMEVQEPAEPTGVNMLSPGSEHLLPEAAERSQRRLLV PANEGDPT 336
:  :		
Qy	294	ETGOOGELAEITGTVTVEXPREFDORLLEOAFAEGCORRLLV PVNDA DSDAD 342
:  :		

RESULT 3  
ID 014708 PRELIMINARY PPT: 200 MM

AC 014798;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DR CYTOXOXYC TRAIL RECEPTOR-3

GN TRAIL-R3.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MACFARLANE M., AHMAD M., SRINIVASULA S.M., FERNANDES-ALNEMRI T.,  
RA COHEN G.M., ALNEMRI E.S.;  
RL J. BIOL. CHEM. 0:0-0(1997).  
DR EMBL; AF020502; G2443820; -.  
SQ SEQUENCE 299 AA; 31759 MW; 59B93A14 CRC32;

Query Match 30.7%; Score 834; DB 2; Length 299;  
 Best Local Similarity 61.9%; Pred. No. 6.40e-139;  
 Matches 130; Conservative 27; Mismatches 50; Indels 3; Gaps 3;

Db 70 RQEVEPVQQTVAPQQQRHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCT 129  
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 60 RQDEVPQQTVAPOQQRRSLKKEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLCT 119

Db 130 VCKSDQHKHSSCTRTDVCQCKEGTRRNNSPEMCRKCSR-CP\$GEVQVSNC\$TSWDQIO 188  
||| ||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Ov 120 VCKSGOTNKHSSCTTRDVCOCKEGSKDOKNSPEMCRCTRCGPGRMVKVSNC\$TPRSDIK 179

Db 189 CVEEFGANATVETPAAEETMNTSPGT PAPA 218

Qy 180 CKNESAASTGKTPAAEETVTTILGMLASP 209

RESULT 4  
ID 014755 PRELIMINARY; PRT; 259 AA.

AC Q14755;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE TRAIL RECEPTOR 3.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER AND SPLEEN;  
RA SCHNEIDER P., BODMER J.-L., THOME M., HOLLER N., HOFMANN K.,  
RA TSCHOPP J.;  
RL FEBS LEFT. 0:0-0(1997).  
DR EMBL; AF016267; G2529565; -.  
SQ SEQUENCE 259 AA; 27365 MW; 3C196935 CRC32;

```

Query Match      30.2%; Score 820; DB 2; Length 259;
Best Local Similarity 69.7%; Pred. No. 4.69e-136;
Matches 122; Conservative 18; Mismatches 34; Indels 1; Gaps 1;

```

Db 5 PTKTLKFVVVIVAVLLPVLAGSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTG 64  
|| || || || || || :||:||:||:||:||:||:|| || || || || || || || || || || || ||  
Cv 25 PTKTLKFVVVIVAVLLPVLAGSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTG 94

Db 65 ACNPCTEGVDYTNASNNEPSCFPCTVCKSDQHKSSCTMTRDVCQCKEGTFRNVSPEM 124

Qy 95 ACNPCTEGVDITYASNNLPSCLLCTVCKSGQTNKSCITTRDTCQC EKGFSQDKNSPEM 154

Qy 155 CRTCRTGCPRGMVKSNCPRSDIKCKNESASSTGKTPAAEETVTTILGMLASP 209

RESULT 5  
ID 015517 PRELIMINARY; PRT; 411 AA.

AC 015517;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE CYTOTOXIC TRAIL RECEPTOR-2.  
GN DR5 OR TRICK2A.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MACFARLANE M., AHMAD M., SRINIVASULA S.M., FERNANDES-ALNEMRI T.,  
RA COHEN G.M., ALNEMRI E.S.;  
RL J. BIOL. CHEM. 0:0-0(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA SCREATON G.R., MONGKOLSAPAYA J., XU X., COWPER A.E., MCMICHAEL A.  
RA BELL A.J.;  
RL CURR. BIOL. 0:0-0(1997).  
.DR EMBL; AF020501; G2443818; -.  
.DR EMBL; AF018657; G2407651; -.  
.SQ SEQUENCE 411 AA; 45127 MW; 579FB4AD CRC32;

RESULT 6  
ID 014720 PRELIMINARY; PRT; 411 AA.

AC 014720;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE DEATH RECEPTOR 5.  
GN DR5.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 97390509.  
RA SHERIDAN J.P., MARSTERS S.A., PITTI R.M., GURNEY A., SKUBATCH M.,  
RA BALDWIN D., RAMAKRISHNAN L., GRAY C.L., BAKER K., WOOD W.I.,  
RA GODDARD A.D., GODOWSKI P., ASHKENAZI A.;  
RL SCIENCE 277:818-821(1997).  
DR EMBL; AF012535; G2338420; -.  
SQ SEQUENCE 411 AA: 45081 MW: 89F2P042 CRC32:

Qy 180 CKNESAASTGKTPAAEETVTTILGMLASPYHYLIIIVLVIIIAVVVVFSCRKKFISY 239  
 Db 215 LKGICSGGGDPERVDR----SSQ-R-PGAEDNVLEIVSI--LQPTQVPEQEMVQE 264  
 ||||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 240 LKGICSGGGGPERVHRLFRRRSCSRVPGAEQNARNETLSNRYLQPTQVSEIQQQE 299  
 Db 265 PAEPTGVNMLSPGESEHLLPAEAERSQRRLLVNPANEGDPT 307  
 || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 300 LAELTGTVEXPERPQRLLQEAEGCQRRRLLPVNDAADSAD 342

RESULT 8  
 ID 000220 PRELIMINARY; PRT; 468 AA.

AC 000220;  
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)  
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE CYTOTOXIC LIGAND TRAIL RECEPTOR.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97238921.  
 RA PAN G., O'ROURKE K., CHINNAIYAN A.M., GENTZ R., EBNER R., NI J.,  
 RA DIXIT V.M.;  
 RL SCIENCE 276:111-113(1997).  
 DR EMBL; U90875; G1945072; -.  
 SQ SEQUENCE 468 AA; 50025 MW; 95AEFC6F CRC32;

Query Match 28.9%; Score 784; DB 2; Length 468;  
 Best Local Similarity 48.8%; Pred. No. 1.06e-128;  
 Matches 168; Conservative 60; Mismatches 79; Indels 37; Gaps 19;

Db 60 GQHGPSAR-ARAGRAGPGRPARAREASPRLRVHKTFKFVV--VGVLLOV-VPSSAATIK--L 113  
 || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 5 GQSVPTASSARAGRYGPARTASGTRPWLLDPKILKFVVFIVAVLLPVVRVDSATIPRQDEV 64  
 Db 114 HDQSIGTQQWEHSPL-GELCPPGSHRSERPGACNRCTEGVGYTNASNLLFACLPCTACKS 172  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 65 PQQTVPQQ-QRSLKEEECPAGSHRSEYTGACNPCTEGVDTIASNNLPSCLLCTVCKS 123  
 Db 173 DEEERSPCITTRNTACQCKPGTFRNDNSAEMCRKCSTGCPGRMVVKDCTPWS DIECVHK 232  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 124 GQTNKSSCTTTRDTCQCCKGSFQDKNSPEMCRCTRCGCPGRMVKSNCPRSDIKCKNE 183  
 Db 233 --ES--GN---GHN-IWIL-VVT----LVPPLLVAVL--IVC--CC---IG--SG-- 267  
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 184 SAASSTGKTPAAEETVTTILGMLASPYHYLIIIVLVIIIAVVVVFSCRKKFISYLKGI 243  
 Db 268 C--GGDPKCMDRVCFWRLG--LLRGPGAEQDNNAHEILNSADSLSTFVSEQMSEQPADL 323  
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 244 CSGGGGGPERVHRLFRRRSCSRVPGAEQNARNETLSNRYLQPTQVSEIQQQELAB 303  
 Db 324 TGTVQSPGEAQCLLGPAEAEAGSQRRRLVPANGADPTETLMF 367  
 || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 304 TGTVEXPPEPQRLLQEAEGCQRRRLLPVNDAADSADISTLL 347

RESULT 9  
 ID 019131 PRELIMINARY; PRT; 471 AA.

AC 019131;  
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR-RECEPTOR I.  
 GN TNF-RI.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; ARTIODACTyla.

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=AORTA;  
 RA LEE E.-K., TAYLOR M.J., KEHRLI M.E.;  
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.  
 DR EMBL; U90937; G2290398; -.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 SQ SEQUENCE 471 AA; 51368 MW; 1D60FF4A CRC32;

Query Match 7.1%; Score 192; DB 4; Length 471;  
 Best Local Similarity 34.6%; Pred. No. 3.21e-14;  
 Matches 36; Conservative 16; Mismatches 41; Indels 11; Gaps 10;

Db 70 NDCP-GPGR-D-TD-CRVCAPIGT-YTALENHLRRLCSRCRDEMFOVEISPVCVDRDTV 124  
 ::| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 81 EECPAGSHRSEYTGACNPCTEGVDTIASNNLPSCLLCTVCKSG--QTNKSSCTTRDVT 138  
 Db 125 CGCRKNQYREYWGEGFRLNCNL-CPNGTVNIP-CQERQDTIC 166  
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 139 QCCEKGSFQD-KNSPEM-CRTCRTGCPGRMVKSNCPRSDIKC 180

RESULT 10  
 ID Q62327 PRELIMINARY; PRT; 459 AA.

AC Q62327;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 mRNA (FRAGMENT).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD;  
 RX MEDLINE; 95178848.  
 RA POWELL E.E., WICKER L.S., PETERSON L.B., TODD J.A.;  
 RL MAMM. GENOME 5:726-727(1994).  
 DR EMBL; X76401; G433831; -.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 FT NON\_TER 1 1  
 FT VARIANT 87 87 S -> T.  
 FT VARIANT 93 93 T -> I.  
 FT VARIANT 268 268 F -> I.  
 FT VARIANT 345 345 S -> F.  
 FT VARIANT 421 421 Y -> C.  
 SQ SEQUENCE 459 AA; 48686 MW; 57791809 CRC32;

Query Match 7.0%; Score 191; DB 10; Length 459;  
 Best Local Similarity 27.6%; Pred. No. 4.71e-14;  
 Matches 29; Conservative 27; Mismatches 44; Indels 5; Gaps 5;

Db 61 CADCEASM-YTQVWNQFRTCLCSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTHSG 119  
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 96 CNPCTEGVDTIASNNLPSCLLCTV-CKSGQTNKSSCTTRDTCQCCEKGSFQD-KNSPE 153  
 Db 120 SCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTD 164  
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 154 MCRTC-RTG-CPRGMVKSNCPRSDIKCKNEAASSTGKTPAAE 196

RESULT 11  
 ID Q85407 PRELIMINARY; PRT; 348 AA.

AC Q85407;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE HOMOLOG OF VACCINIA VIRUS CDS B28R.  
 GN G2R.  
 OS VARIOLA VIRUS.  
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPHOXVIRINAE;



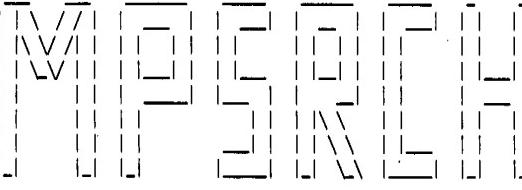
ID Q14293 PRELIMINARY; PRT; 314 AA.

AC Q14293;  
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE PAS SOLUBLE PROTEIN.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95181785.  
RA CASCINO I., FIUCCI G., PAPOFF G., RUBERTI G.;  
RL J. IMMUNOL. 154:2706-2713(1995).  
DR EMBL; 247993; G695539; -.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
SQ SEQUENCE 314 AA; 35386 MW; F39D50D5 CRC32;

Query Match 6.7%; Score 182; DB 2; Length 314;  
Best Local Similarity 35.6%; Pred. No. 1.44e-12;  
Matches 32; Conservative 18; Mismatches 35; Indels 5; Gaps 4;

Db 82 CVPCQEGKEYTDKAHFSSKRRRCRLCDEGHGLEVEINCTRTQNTKCRCKPNFCNSTVCE 141  
| | | | :|| :: :| | :| | : : || |::| || | | : | |  
Qy 96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGQT-N-KSSCTTRDTVCQCEKGSFQDKNSPE 153  
  
Db 142 HCDPC-TKCEHGIK--ECLTLSNTKCKEE 168  
| | | | :|| | :|| | : |||:  
Qy 154 MCRTCRTGCPGMVKVSNCPRSDIKCKNE 183

Search completed: Thu May 14 16:49:06 1998  
Job time : 52 secs.

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 (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 14 16:50:10 1998; MasPar time 11.05 Seconds  
 522.069 Million cell updates/sec

Tabular output not generated.

Title: >US-08-918-874-1  
 Description: (1-386) from US08918874.pep  
 Perfect Score: 2715  
 Sequence: 1 MGLWQSVPTASSARAGRYP.....VGSEKLFYEEDEAGSATSC 386

Scoring table: PAM 150  
 Gap 11

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: a-geneseq31  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
 14:part14 15:part15 16:part16 17:part17 18:part18  
 19:part19 20:part20 21:part21 22:part22 23:part23  
 24:part24 25:part25 26:part26

Statistics: Mean 34.398; Variance 153.278; scale 0.224

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	%					
No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	201	7.4	600	14	R78610	Expression vector pME	1.65e-07
2	195	7.2	474	2	R11142	TNF-R deduced from mT	5.19e-07
3	191	7.0	335	5	R28084	Human cell surface an	1.1le-06
4	191	7.0	335	14	R78606	Human Fas protein.	1.1le-06
5	191	7.0	335	17	R92528	hFas from plasmid pCE	1.1le-06
6	191	7.0	335	18	R99681	Human Fas antigen.	1.1le-06
7	186	6.9	355	15	R85073	Cowpox virus T2-equiv	2.87e-06
8	188	6.9	592	17	R92527	Fas antigen #2.	1.97e-06
9	187	6.9	600	17	R92526	Fas antigen #1.	2.38e-06
10	184	6.8	576	14	R78613	Expression vector pME	4.19e-06
11	182	6.7	314	18	R99682	Human Fas soluble ant	6.12e-06
12	182	6.7	314	13	R76238	Fas-delta-TM.	6.12e-06
13	179	6.6	159	4	R24083	Truncated TNF-alpha 5	1.08e-05
14	180	6.6	326	5	R27866	Myxoma virus T2 prote	8.91e-06
15	180	6.6	326	15	R85072	Myxoma virus T2 prote	8.91e-06
16	177	6.5	169	14	R78612	Plasmid fragment pME1	1.57e-05
17	176	6.5	285	26	W33359	TBP(20-190)/hCG-alpha	1.89e-05
18	177	6.5	327	17	R92530	mFas sequence.	1.57e-05
19	177	6.5	327	14	R78611	Murine Fas antigen ex	1.57e-05

20	177	6.5	327	8	R41688	Murine Fas.	1.57e-05
21	173	6.4	161	5	R27496	Native 30 kD TNF inhi	3.31e-05
22	173	6.4	168	4	R24084	Truncated TNF-alpha 5	3.31e-05
23	173	6.4	199	4	R24080	Truncated TNF-alpha 5	3.31e-05
24	173	6.4	256	26	W33357	TBP(20-161)/hCG-alpha	3.31e-05
25	173	6.4	307	26	W33358	TBP(20-161)/hCG-beta	3.31e-05
26	173	6.4	309	13	R70108	TNF-R-GBPH fusion pro	3.31e-05
27	173	6.4	336	26	W33360	TBP(20-190)/hCG-beta	3.31e-05
28	173	6.4	371	2	R07449	Tumour Necrosis Facto	3.31e-05
29	173	6.4	451	13	R70107	TNF-R-GBP 130 fusion	3.31e-05
30	173	6.4	455	14	R75084	p55 TNF-R.	3.31e-05
31	173	6.4	455	4	R24000	TNF-alpha 55kD recept	3.31e-05
32	173	6.4	455	2	R11082	Human 55kD TNF-bindin	3.31e-05
33	173	6.4	455	2	R07451	Human Tumour Necrosis	3.31e-05
34	173	6.4	455	2	R10986	30kD TNF inhibitor pr	3.31e-05
35	173	6.4	455	3	R12550	Type I TNF receptor.	3.31e-05
36	173	6.4	455	8	R42059	Lambda derived TNF-R.	3.31e-05
37	173	6.4	455	4	R20787	TNF-alpha binding pro	3.31e-05
38	173	6.4	547	13	R70104	TNF-R-GBPH fusion pro	3.31e-05
39	173	6.4	884	13	R70109	TNF-R-GBP 130 fusion	3.31e-05
40	173	6.4	900	13	R70103	TNF-R-GBP 130 fusion	3.31e-05
41	173	6.4	1245	13	R70106	TNF-R-PI. vivax Duffy	3.31e-05
42	173	6.4	1604	13	R70105	TNF-R-BBA 175 fusion	3.31e-05
43	167	6.2	393	20	R99948	Mutated OCIF, OCIF-CB	1.01e-04
44	167	6.2	399	20	R99942	Mutated OCIF, OCIF-CL	1.01e-04
45	169	6.2	401	20	R99933	Mutated OCIF, OCIF-C2	6.97e-05

#### ALIGNMENTS

RESULT	1
ID	R78610 standard; Protein; 600 AA.
AC	R78610;
DT	19-FEB-1996 (first entry)
DE	Expression vector pME18S/hFas.EXT-AIC2A protein prod..
KW	Expression vector; pME18S/hFas.EXT-AIC2A; human Fas antigen;
KW	extracellular; region; AIC2A; soluble membrane protein;
KW	antibody production; diseases; treatment; prevention.
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	peptide 1..16
FT	/label= sig_peptide
FT	peptide 17..600
FT	/label= mat_peptide
PN	J07115988-A.
PD	09-MAY-1995.
PF	26-OCT-1993; 267644.
PR	26-OCT-1993; JP-267644.
PA	(NISB ) JAPAN TOBACCO INC.
DR	WPI; 95-202847/27.
DR	N-PSDB; Q95301.
PT	Preparation of soluble membrane proteins - for their use in antibody
PT	production for the treatment and prevention of related diseases
PS	Claim 10; Pages 28-30; 51pp; Japanese.
CC	R78610 is the protein prod. of the expression vector pME18S/human Fas
CC	antigen.extracellular region-AIC2A. The expression vector was used for
CC	the prodn. of recombinant soluble membrane proteins. The proteins can
CC	be used in antibody prodn. for the treatment and prevention of related
CC	diseases.
SQ	Sequence 600 AA;
Query	Match 7.4%; Score 201; DB 14; Length 600;
Best Local Similarity	35.8%; Pred. No. 1.65e-07;
Matches	38; Conservative 22; Mismatches 40; Indels 6; Gaps 5;
Db	82 cvpcqeqkeytdkahfsskrrcrcldceghgleinecntrqntkrckpnffcnstvce 141         :   :: :     :   : :   :   :   :   :   :   :   :   :   :   :   :
Qy	96 CNPCTEGVDYTIASNNLPSCLLCVCKSGQT-N-KSSCTTTRDTVCQCEKGSFQDKNSPE 153
Db	142 hdpcc-tkcehgjik--ectltsntkceegsrsavaat-eeeety 183         :   ::   :     :   :   :   :   :   :   :   :   :   :   :   :
Qy	154 MCRTCRTGCPGRMVKVSNCPRSDIKCKNESAASSTGKTPAAETV 199

**RESULT** 2  
ID R11142 standard; Protein; 474 AA.  
AC R11142;  
DT 24-MAY-1991 (first entry)  
DE TNF-R deduced from mTNF-R clone 11.  
KW Tumour necrosis factor receptor; immune response; inflammation;  
KW cachexia; septic shock.  
OS Mus musculus strain C57BL/6.  
FH Key Location/Qualifiers  
FT peptide 1..22  
FT /label= signal sequence  
FT domain 234..265  
FT /label= transmembrane region  
PN EP-418014-A.  
PD 20-MAR-1991.  
PF 10-SEP-1990; 309875.  
PR 11-SEP-1989; US-405370.  
PR 13-OCT-1989; US-421417.  
PR 10-MAY-1990; US-523635.  
PA (IMMU-) IMMUNEX CORP.  
PI Smith CA, Goodwin RG, Beckmann PM;  
DR WPI; 91-082230/12.  
DR N-PSDB; Q10991.  
PT New tumour necrosis factor -alpha and -beta receptors - and DNA  
PT encoding these used to regulate immune responses in treatment of  
PT cachexia, septic shock or side-effects of cytokine therapy.  
PS Disclosure; Fig 3; 41pp; English.  
CC The sequence was deduced from a clone isolated from library prep'd.  
CC from a murine T helper cell line, 7B9.  
CC See also R11141.  
SQ Sequence 474 AA;

```

Query Match          7.28; Score 195; DB 2; Length 474;
Best Local Similarity 28.6%; Pred. No. 5.19e-07;
Matches 30; Conservative 27; Mismatches 43; Indels 5; Gaps 5;

b    76 cadceasm-ytqvwngftclscsscttdqveiractkqgnrvaceagrycdlkthsg 134
| | | : || | : || | : || | : || | : || | : || | : || | : || | :
y    96 CNPCTEGVDYTIASNNLPSCLCTV-CKSGQTNKSSCTTTRDTCVCQCEKGSFQD-KNSPE 153

b    135 srqcgmrlskcgpgfgyassrapngnvlckacapgtfsdttsst 179
| | | | : | | : | : || : || : | : | : | : | : | : | : | : |
y    154 MCRTC-RTG-CPRGMVKVSNCTPRSDIKCKNESAASTGKTPAAE 196

```

```

RESULT      3
ID   R28084 standard; Protein; 335 AA.
AC   R28084;
DT   12-MAR-1993 (first entry)
DE   Human cell surface antigen.
KW   Fas antigen; apoptosis; pF58; NGFR/TNFR family
OS   Homo sapiens.
FH   Key          Location/Qualifiers
FT   peptide      1..16
FT                   /label= signal
FT   protein       17..335
FT                   /label= Fas_antigen
FT   modified_site 118..120
FT                   /label= N-glycosylation_site
FT                   /note= "putative"
FT   modified_site 136..138
FT                   /label= N-glycosylation_site
FT                   /note= "putative"
FT   domain        174..190
FT                   /label= transmembrane
FT   domain        17..173
FT                   /label= extracellular
FT                   /note= "cysteine-rich"
FT   domain        191..335
FT                   /label= cytoplasmic
FT
PN   EP-510691-A.
PD   28-OCT-1992.

```

PF 24-APR-1992; 107060.  
PR 26-APR-1991; JP-125234.  
PA (OSAB-) OSAKA BIOSCIENCE INST.  
PI Itoh N, Nagata S, Yonehara S;  
DR WPI; 92-358914/44.  
DR N-PSDB; Q29959.  
PT DNA encoding human cell surface antigen - used to clarify  
PT apoptosis mechanism of various types of cell, and to prepare  
PT monoclonal antibodies that react with tumour cells expressing Fas  
PS Claim 3; Fig 1 and 2; 27pp; English.  
CC The Fas antigen is implicated in apoptosis. A cDNA clone encoding  
CC the antigen was isolated (pF58) and the amino acid sequence of Fas  
CC was deduced from it. The mature protein has a calculated mol.wt. of  
CC 36,000 and is a member of the NGFR/TNFR family of cell-surface  
CC membrane proteins. The inventors claim a protein comprising at  
CC least the extracellular domain of Fas antigen.  
SQ Sequence 335 AA;

```

Query Match          7.0%; Score 191; DB 5; Length 335;
Best Local Similarity 35.1%; Pred. No. 1.11e-06;
Matches   34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;

Db    82 cypcqegekeytdkahfsskcrclrcdeghleveinctrqntkrckpnffcnstvce 141
      ||||| :|| :: :|| | :|| | : : ||| :|| | : | : |
Qy    96 CNPCTEGVDTIASNNLPSCLLCVCKSGQI-N-KSSCTTTRDTCVQCCKGSFQDKNSPE 153

Db    142 hcdpct-kcehgii--ectltsntkckeegrsrlng 175
      | | | | :||| :|| | :|| | :||| :|| | :
Qy    154 MCRTCRTGCPGRMVKVSNCNTPRSIDKCKNESAASSTG 190

```

RESULT 4  
ID R78606 standard; Protein; 335 AA.  
AC R78606;  
DT 19-FEB-1996 (first entry)  
DE Human Fas protein.  
KW Plasmid pf58; human Fas cDNA; soluble membrane protein;  
KW antibody production; diseases; treatment; prevention.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT peptide 1..16  
FT /label= sig\_peptide  
FT peptide 17..335  
FT /label= mat\_peptide  
PN J07115988-A.  
PD 09-MAY-1995.  
PF 26-OCT-1993; 267644.  
PR 26-OCT-1993; JP-267644.  
PA (NISB ) JAPAN TOBACCO INC.  
DR WPI; 95-202847/27.  
DR N-PSDB; Q95297.  
PT Preparation of soluble membrane proteins - for their use in antibody  
PT production for the treatment and prevention of related diseases  
PS Example 1; Pages 15-17; 51pp; Japanese.  
CC R78606 (human Fas protein) is encoded by the plasmid pf58 which  
CC contains hFas cDNA. The plasmid was used in the construction of an  
CC expression vector for the prodn. of recombinant soluble membrane  
CC proteins. The proteins can be used in antibody prodn. for the  
CC treatment and prevention of related diseases.  
SQ Sequence 335 AA;

```

Query Match          7.0%; Score 191; DB 14; Length 335;
Best Local Similarity 35.1%; Pred. No. 1.1le-06;
Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;

Db    82 cypcqgegkeytdkahfsskrrcrlcdeghgleveinctrqntkrckpnffcnstvce 141
      ||||| :|| :: : | : | : | : | : | : | : | : | : | : | : |
Qy    96 CNPCTEGVDYTIASSNLPSCLLCTVCKSGQT-N-KSSCTTTRDTCVQCCKGSFQDKNSPE 153

Db    142 hcdpcktcehgiik--ectltsntkceegrsnl 175
      | | | | :| :| :| : | : | : | : | : | : |
Qy    154 MCRTCRTGCPGRGMVKVSNTPRSDIKCKNESAASSTG 190

```

RESULT 5  
 ID R92528 standard; Protein; 335 AA.

AC R92528;  
 DT 06-SEP-1996 (first entry)

DE hFas from plasmid pCEV4/hFas.

KW Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;  
 KW rheumatoid arthritis; serum; systemic lupus erythematosus.

OS Synthetic.

FH Key Location/Qualifiers

FT peptide 1..16

FT protein /note= "hFas signal peptide"

FT protein 17..335

FT protein /note= "mature hFas"

PN W09601277-A1.

PD 18-JAN-1996.

PF 03-MAR-1995; J00349.

PR 06-JUL-1994; JP-154706.

PR 14-FEB-1995; JP-025637.

PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.

PA (NISB ) JAPAN TOBACCO INC.

PI Hachiya T, Noguchi J, Yonehara S;

DR WPI; 96-087635/09.

DR N-PSDB; T16303.

PT Immunoassay method for soluble Fas antigen in body fluids - for  
 PT diagnosis of auto-immune diseases such as rheumatoid arthritis and

PT systemic lupus erythematosus

PS Example 8; Page 49-52; 124pp; Japanese.

CC This sequence represents the sequence for the human Fas antigen contained  
 CC within the plasmid pCEV4/hFas. The soluble Fas antigen is included in  
 CC the immunoassay kit of the invention. The kit is for the assay of  
 CC soluble Fas antigen and contains an immobilised anti-soluble Fas  
 CC monoclonal antibody, as well as the standard soluble Fas antigen  
 CC represented by this sequence. The assay is simple and has high accuracy,  
 CC high sensitivity, and is capable of assaying a number of different  
 CC specimens at the same time. The immunoassay is used on biological  
 CC samples (such as serum) and is useful for diagnosis of autoimmune  
 CC diseases such as rheumatoid arthritis or systemic lupus erythematosus  
 CC (SLE).

SQ Sequence 335 AA;

Query Match 7.0%; Score 191; DB 17; Length 335;  
 Best Local Similarity 35.1%; Pred. No. 1.1e-06;  
 Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;

Db 82 cvpcqegkeytdkahfsskcrccrlcdeghgleveinctrqntkrckpnffcnstvce 141  
 ||||| :|| :: :|| | :| :| :|| :|| :|| :|| :|

Qy 96 CNPCTEGVDYTIASNNLPSCLLCVCKSGQT-N-KSSCTTRDTCQCEKGSFQDKNSPE 153

Db 142 hcpsc-tkcehgiik--ectltsntkckeegrsnlg 175  
 ||||| :|| :|| | :| :|| :|| :|| :|| :|

Qy 154 MCRTCRTGCPGRGMVKVSNCPRSDIKCKNESAASTG 190

RESULT 6

ID R99681 standard; Protein; 335 AA.

AC R99681;

DT 10-OCT-1996 (first entry)

DE Human Fas antigen.

KW Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;  
 KW angioimmunoblastic lymphadenopathy; AILD.

OS Homo sapiens.

FH Key Location/Qualifiers

FT peptide 1..16

FT protein /label= Sig\_peptide

FT protein 17..335

FT domain 17..173

FT domain /label= Extracellular\_domain

FT domain 174..190

FT domain /label= Transmembrane\_domain

FT domain 191..335

FT domain /label= Cytoplasmic\_tail

PN W09620206-A1.

PD 04-JUL-1996.

PF 22-DEC-1995; U17083.

PR 23-DEC-1994; US-371263.

PA (UABR-) UAB RES FOUND.

PI Cheng J, Liu C, Mountz JD, Zhou T;

DR WPI; 96-321796/32.

DR N-PSDB; T34526.

PT Natural, soluble form of Fas antigen secreted by human cells is

PT result of alternative mRNA processing - used to diagnose

PT Fas-associated disease, e.g. systemic lupus erythematosus

PS Disclosure; Page 109-111; 152pp; English.

CC A cDNA clone (T34526) codes for a membrane receptor-like protein,

CC Fas antigen (R99681). It was isolated from cDNA derived from the

CC peripheral blood mononuclear cells of systemic lupus erythematosus

CC (SLE) and angioimmunoblastic lymphadenopathy (AILD) patients. 4

CC Soluble variants (R99682-85) were identified of the Fas antigen.

CC These arose by alternative splicing of Fas gene transcripts. The

CC Fas variants were present at higher levels in SLE and AILD patients

CC than the non-soluble Fas antigen.

SQ Sequence 335 AA;

Query Match 7.0%; Score 191; DB 18; Length 335;  
 Best Local Similarity 35.1%; Pred. No. 1.1e-06;  
 Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;

Db 82 cvpcqegkeytdkahfsskcrccrlcdeghgleveinctrqntkrckpnffcnstvce 141  
 ||||| :|| :: :|| | :| :| :|| :|| :|| :|| :|

Qy 96 CNPCTEGVDYTIASNNLPSCLLCVCKSGQT-N-KSSCTTRDTCQCEKGSFQDKNSPE 153

Db 142 hcpsc-tkcehgiik--ectltsntkckeegrsnlg 175  
 ||||| :|| :|| | :| :|| :|| :|| :|| :|

Qy 154 MCRTCRTGCPGRGMVKVSNCPRSDIKCKNESAASTG 190

RESULT 7

ID R85073 standard; Protein; 355 AA.

AC R85073;

DT 16-APR-1996 (first entry)

DE Cowpox virus T2-equivalent protein.

KW Cowpox virus; immunosuppressive; cytokine antagonist;

KW tumour necrosis factor antagonist; therapeutic; cachexia;

KW septic shock.

OS Cowpox virus.

PN US5464938-A.

PD 07-NOV-1995.

PF 18-AUG-1994; 292549.

PR 19-OCT-1992; US-963330.

PA (IMMV ) Immunex Corp.

PI Goodwin RG, Smith CA

DR WPI; 95-402861/51.

DR N-PSDB; T02472.

PT New soluble viral proteins that bind tumour necrosis factor - for  
 PT treating cachexia, septic shock, side effects of TNF therapy etc.,  
 PT also useful in assays, affinity purifcn. and antibody prodn.

PS Claim 1; Columns 35-38; 21pp; English.

CC The cowpox virus T2-equivalent protein is a soluble viral protein

CC which binds tumour necrosis factor (TNF), thus inhibiting TNF

CC binding to its receptor. T2 protein is useful (when administered

CC by injection or infusion from sustained release implants, etc.) for

CC treating TNF associated toxicity e.g. side effects of using TNF as

CC an antitumour agent or in cases of cachexia and septic shock where

CC TNF production is excessive.

SQ Sequence 355 AA;

Query Match 6.9%; Score 186; DB 15; Length 355;  
 Best Local Similarity 32.6%; Pred. No. 2.87e-06;  
 Matches 31; Conservative 22; Mismatches 37; Indels 5; Gaps 4;

Db 58 ktntntqtpcasdt-ftsrnhhlpac1scngrcdsnqvetsncnhrnidcapgyc 116  
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:

Qy 89 RSEYTGACNPCTEGVDYTIASNNLPSCLLCV-CKSGQTNKSSCTTRDTCQCEKGSFQ 147

Db 117 flkgssgokacvsqtkcgisyy-vsghptgdvvc 150  
   ::|::|::|::|::|::|::|::|:  
 Qy 148 DKNSPEMCRTC--RTGCPGRGMVKVSNCTPRSDIKC 180

## RESULT 8

ID R92527 standard; Protein; 592 AA.  
 AC R92527;  
 DT 06-SEP-1996 (first entry)  
 DE Fas antigen #2.  
 KW Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;  
 KW rheumatoid arthritis; serum; systemic lupus erythematosus.  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT peptide 1..21  
 FT /note= "signal peptide"  
 FT protein 22..592  
 FT /note= "mature Fas antigen #2"  
 PN WO9601277-A1.

PD 18-JAN-1996.  
 PF 03-MAR-1995; J00349.  
 PR 06-JUL-1994; JP-154706.  
 PR 14-FEB-1995; JP-025637.  
 PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.  
 PA (NISB ) JAPAN TOBACCO INC.  
 PI Hachiya T, Noguchi J, Yonehara S;  
 DR WPI; 96-087635/09.  
 DR N-PSDB; T16301.

PT Immunoassay method for soluble Fas antigen in body fluids - for  
 PT diagnosis of auto:immune diseases such as rheumatoid arthritis and  
 PT systemic lupus erythematosus  
 PS Claim 11; Page 87-91; 124pp; Japanese.  
 CC R92526 and R92527 represent soluble Fas antigens. These soluble Fas  
 CC antigen is included in the immunoassay kit of the invention. The kit is  
 for the assay of soluble Fas antigen and contains an immobilised  
 CC anti-soluble Fas monoclonal antibody, as well as one of these standard  
 CC soluble Fas antigens. The assay is simple and has high accuracy, high  
 CC sensitivity, and is capable of assaying a number of different specimens  
 at the same time. The immunoassay is used on biological samples (such as  
 CC serum) and is useful for diagnosis of autoimmune diseases such as  
 CC rheumatoid arthritis or systemic lupus erythematosus (SLE).  
 SQ Sequence 592 AA;

Query Match 6.9%; Score 188; DB 17; Length 592;  
 Best Local Similarity 31.8%; Pred. No. 1.97e-06;  
 Matches 35; Conservative 26; Mismatches 42; Indels 7; Gaps 7;

Db 75 tptcapctegkey-mdknhypdkcrctlcdeehglevetnctltqntkckcpdfycds 133  
   | :| ||||| :| :| :| | ||| : : :||| ||| :| :|  
 Qy 93 TGACNPCTEGVDYTIASNNLPS-CLLCTVCKSGQT-N-KSSCTTRDTVCQCEKGSFQDK 149

Db 134 pgcehcvrc-ascehgtle-p-ctatsntncrkgsprnrlwhvteeeetv 180  
   :| | :| :| :| : :||| :| :| :| :| :| :| :|  
 Qy 150 NSPEMCRTCRTGCPGRGMVKVSNCTPRSDIKCNESAASSTGKTPAAETV 199

## RESULT 9

ID R92526 standard; Protein; 600 AA.  
 AC R92526;  
 DT 06-SEP-1996 (first entry)  
 DE Fas antigen #1.  
 KW Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;  
 KW rheumatoid arthritis; serum; systemic lupus erythematosus.  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT peptide 1..16  
 FT /note= "signal peptide"  
 FT protein 17..600  
 FT /note= "mature Fas antigen #1"  
 PN WO9601277-A1.  
 PD 18-JAN-1996.  
 PF 03-MAR-1995; J00349.  
 PR 06-JUL-1994; JP-154706.

PR 14-FEB-1995; JP-025637.  
 PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.  
 PA (NISB ) JAPAN TOBACCO INC.  
 PI Hachiya T, Noguchi J, Yonehara S;  
 DR WPI; 96-087635/09.  
 DR N-PSDB; T16300.  
 PT Immunoassay method for soluble Fas antigen in body fluids - for  
 PT diagnosis of auto:immune diseases such as rheumatoid arthritis and  
 PT systemic lupus erythematosus  
 PS Claim 13; Page 73-77; 124pp; Japanese.  
 CC R92526 and R92527 represent soluble Fas antigens. These soluble Fas  
 CC antigen is included in the immunoassay kit of the invention. The kit is  
 for the assay of soluble Fas antigen and contains an immobilised  
 CC anti-soluble Fas monoclonal antibody, as well as one of these standard  
 CC soluble Fas antigens. The assay is simple and has high accuracy, high  
 CC sensitivity, and is capable of assaying a number of different specimens  
 at the same time. The immunoassay is used on biological samples (such as  
 CC serum) and is useful for diagnosis of autoimmune diseases such as  
 CC rheumatoid arthritis or systemic lupus erythematosus (SLE).  
 SQ Sequence 600 AA;

Query Match 6.9%; Score 187; DB 17; Length 600;  
 Best Local Similarity 34.9%; Pred. No. 2.38e-06;  
 Matches 37; Conservative 22; Mismatches 41; Indels 6; Gaps 5;

Db 82 cvpsgegkeytdkahfsskcrccrlcdeghgleveinctrqntkcrckpnffcnstvce 141  
   | | ||| :| :: :| | :| :| :| :| :| :| :| :|  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGQT-N-KSSCTTRDTVCQCEKGSPQDKNSPE 153

Db 142 hcdpc-tkcehgikey-ectltsntkckeegrsavaat-eeeetv 183  
   | | | :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 154 MCRTCRTGCPGRGMVKVSNCTPRSDIKCNESAASSTGKTPAAETV 199

## RESULT 10

ID R78613 standard; Protein; 576 AA.  
 AC R78613;  
 DT 20-FEB-1996 (first entry)  
 DE Expression vector pME18S/mFas.EXT-AIC2A protein prod..  
 KW Expression vector; pME18S/mFas.EXT-AIC2A; murine Fas antigen;  
 KW extracellular; region; AIC2A; soluble membrane protein;  
 KW antibody production; diseases; treatment; prevention.  
 OS Mus musculus.

PN J07115988-A.  
 PD 09-MAY-1995.  
 PF 26-OCT-1993; 267644.  
 PR 26-OCT-1993; JP-267644.  
 PA (NISB ) JAPAN TOBACCO INC.  
 DR WPI; 95-202847/27.  
 DR N-PSDB; Q95306.  
 PT Preparation of soluble membrane proteins - for their use in antibody  
 PT production for the treatment and prevention of related diseases  
 PS Claim 10; Pages 36-38; 51pp; Japanese.  
 CC R78613 is the protein prod. of the expression vector pME18S/murine Fas  
 CC antigen.extracellular region-AIC2A. The expression vector was used for  
 CC the prodn. of recombinant soluble membrane proteins. The proteins can  
 CC be used in antibody prodn. for the treatment and prevention of related  
 CC diseases.  
 SQ Sequence 576 AA;

Query Match 6.8%; Score 184; DB 14; Length 576;  
 Best Local Similarity 30.3%; Pred. No. 4.19e-06;  
 Matches 33; Conservative 26; Mismatches 45; Indels 5; Gaps 5;

Db 75 tptcapctegkeymdknhyadkcrctlcdeehglevetnctltqntkckcpdfycdsp 134  
   | :| ||||| :| :: :| | :| :| :| :| :| :| :|  
 Qy 93 TGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQT-N-KSSCTTRDTVCQCEKGSFQDK 150

Db 135 gcehcvrc-ascehgtle-p-ctatsntncrkgsprnrlwhvteeeetv 180  
   :| | :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 151 SPEMCRTCRTGCPGRGMVKVSNCTPRSDIKCNESAASSTGKTPAAETV 199

RESULT 11  
 ID R99682 standard; Protein; 314 AA.  
 AC R99682;

DT 10-OCT-1996 (first entry)  
 DE Human Fas soluble antigen Fas del1.  
 KW Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;  
 KW angioimmunoblastic lymphadenopathy; AILD.  
 OS Homo sapiens.

FH Key Location/Qualifiers  
 FT peptide 1..16  
 FT /label= Sig\_peptide  
 FT protein 17..314  
 FT /label= Mat\_protein  
 FT /note= "soluble Fas del1 antigen"  
 FT domain 17..168  
 FT /label= Extracellular\_domain  
 FT /note= "the 5 C-terminal residues of the  
 Fas antigen extracellular domain are  
 deleted in Fas del1"  
 FT domain 169..314  
 FT /label= Cytoplasmic\_domain  
 FT peptide 164..173  
 FT /note= "preferred peptide from breakpoint region  
 (claim 4, page 132)"  
 FT peptide 164..174  
 FT /note= "preferred peptide from breakpoint region"  
 FT peptide 161..171  
 FT /note= "preferred peptide from breakpoint region"  
 PN W09620206-A1.  
 PD 04-JUL-1996.  
 PF 22-DEC-1995; U17083.  
 PR 23-DEC-1994; US-371263.  
 PA (UABR-) UAB RES FOUND.  
 PI Cheng J, Liu C, Mountz JD, Zhou T;  
 DR WPI; 96-321796/32.  
 DR N-PSDB; T34527.

PT Natural, soluble form of Fas antigen secreted by human cells is  
 PT result of alternative mRNA processing - used to diagnose  
 PT Fas-associated disease, e.g. systemic lupus erythematosus  
 PS Claim 4; Page 114-16; 152pp; English.  
 CC A natural, soluble Fas antigen variant (R99682), designated Fas  
 CC del1, and other Fas variants (R99683-85) are derived by alternative  
 CC splicing of Fas gene transcripts. A cDNA clone (T34527) coding for  
 CC the variant was obtnd. from human peripheral blood mononuclear cells.  
 CC The Fas del1 variant lacks the transmembrane domain of insoluble  
 CC Fas antigen (R99681). Recombinant del1 variant, or fragments of  
 CC it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells.  
 CC Detection of increased levels of soluble forms of Fas antigen can  
 CC be used to diagnose autoimmune diseases, esp. systemic lupus  
 CC erythematosus and angioimmunoblastic lymphadenopathy.  
 SQ Sequence 314 AA;

Query Match 6.7%; Score 182; DB 18; Length 314;  
 Best Local Similarity 35.6%; Pred. No. 6.12e-06;  
 Matches 32; Conservative 18; Mismatches 35; Indels 5; Gaps 4;

Db 82 cvpcqeqkeytdkahfsskrrcrlcdeghgleveinctrqntkrckpnffcnstvce 141  
 ||| ||| :|| :: :|| | :| : :|| |::| :|| | :| |  
 Qy 96 CNPCTEGVDYTIASNLLPSCLLCTVCKSGQT-N-KSSCTTTRDTVCQCEKGSFQDKNSPE 153

Db 142 hcdpc-tkcehgiik--ectltsntkckee 168  
 ||| ||| :||| :|| | :| |||:  
 Qy 154 MCRTCRTGCPGRGMVKVSNCPRSDIKCKNE 183

RESULT 12  
 ID R76238 standard; Protein; 314 AA.  
 AC R76238;

DT 06-NOV-1995 (first entry)  
 DE Fas-delta-TM.  
 KW Fas-delta-TM; transmembrane deletion; apoptosis; antibody;  
 KW adoptive immunotherapy; transgenic animal.  
 OS Homo sapiens.

FH Key Location/Qualifiers  
 FT peptide 1..16  
 FT /label= Sig\_peptide  
 PN W09513701-A.  
 PD 26-MAY-1995.  
 PF 15-NOV-1994; U13173.  
 PR 15-NOV-1993; US-152443.  
 PA (LXRB-) LXR BIOTECHNOLOGY INC.  
 PI Barr PJ, Kiefer MC, Shapiro JP;  
 DR WPI; 95-200120/26.  
 DR N-PSDB; Q93879.  
 PT New nucleic acid encoding Fas protein without its trans-membrane region  
 PT - and related vectors, transformed cells, transgenic animals, protein and  
 PT antibodies, useful for control of Fas mediated apoptosis  
 PS Claim 9; Fig.3-1 to 3-4; 38pp; English.  
 CC mRNA was obtnd. from human lymphocytes and PCR was used to make  
 CC cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane  
 CC region) mRNA. The PCR product was ligated into pBluescript and the  
 CC recombinant plasmid was used to transfet E. coli DH5-alpha cells. The  
 CC insert sequence of pBluescript-Fas-delta-TM encoded the protein  
 CC given in R76238.  
 SQ Sequence 314 AA;

Query Match 6.7%; Score 182; DB 13; Length 314;  
 Best Local Similarity 35.6%; Pred. No. 6.12e-06;  
 Matches 32; Conservative 18; Mismatches 35; Indels 5; Gaps 4;

Db 82 cvpcqeqkeytdkahfsskrrcrlcdeghgleveinctrqntkrckpnffcnstvce 141  
 ||| ||| :|| :: :|| | :| : :|| |::| :|| | :| |  
 Qy 96 CNPCTEGVDYTIASNLLPSCLLCTVCKSGQT-N-KSSCTTTRDTVCQCEKGSFQDKNSPE 153

Db 142 hcdpc-tkcehgiik--ectltsntkckee 168  
 ||| ||| :||| :|| | :| |||:  
 Qy 154 MCRTCRTGCPGRGMVKVSNCPRSDIKCKNE 183

RESULT 13  
 ID R24083 standard; Protein; 159 AA.  
 AC R24083;  
 DT 05-NOV-1992 (first entry)  
 DE Truncated TNF-alpha 55KD receptor.  
 KW tumour necrosis factor alpha; extracellular binding domain;  
 KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
 KW malaria; viral meningitis; graft versus host disease;  
 KW autoimmune disease; rheumatoid arthritis.  
 OS Homo sapiens.  
 PN W09207076-A.  
 PD 30-APR-1992.  
 PF 18-OCT-1991; G01826.  
 PR 18-OCT-1990; GB-022648.  
 PA (CHAR-) CHARING CROSS SUNLEY RES CENT.  
 PI Brennan FM, Feldmann M, Gray PW, Turner MJC;  
 DR WPI; 92-167156/20.  
 DR N-PSDB; Q24444.

PT New polypeptide capable of binding human TNF alpha - comprises  
 PT first three cysteine-rich subdomains of TNF alpha receptor for  
 PT treating autoimmune disease, septic shock, HIV etc.  
 PS Example 1; Fig 10; 43pp; English.  
 CC This sequence is a truncated TNF-alpha receptor derivative  
 CC as encoded in pdeltaIII. This was produced as described in  
 CC Q24444. This derivative lacks the third cysteine rich subdomain.  
 CC It could be used to regulate TNF-alpha mediated responses by binding  
 CC and sequestering human TNF-alpha e.g. in the treatment of pulmonary  
 CC diseases, septic shock, HIV infection, malaria, viral meningitis,  
 CC graft versus host disease and autoimmune diseases, esp. rheumatoid  
 CC arthritis.  
 CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8  
 SQ Sequence 159 AA;

Query Match 6.6%; Score 179; DB 4; Length 159;  
 Best Local Similarity 41.2%; Pred. No. 1.08e-05;  
 Matches 28; Conservative 7; Mismatches 30; Indels 3; Gaps 3;

Db 81 crecesg-sftasenhlrhclscskrkemggveissctvdrdtvctchagfflrenevc 139  
   |  |  |  |  |  |  |  |  |  |  |  |  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCCTVC-KS-GQTNKSSCTTRDTVCQCEKGSFQDKNSPE 153  
 Db 140 scsnckks 147  
   |  |  |  |:  
 Qy 154 MCRTCRTG 161

RESULT 14  
 ID R27866 standard; Protein; 326 AA.  
 AC R27866;  
 DT 11-MAR-1993 (first entry)  
 DE Myxoma virus T2 protein.  
 KW Polymerase chain reaction; TNF antagonist; tumour necrosis factor.  
 OS Myxoma virus.  
 PN WO9217583-A.  
 PD 15-OCT-1992.  
 PF 29-MAR-1991; U02207.  
 PR 29-MAR-1991; WO-U22076.  
 PA (IMMV ) IMMUNEX CORP.  
 PI Goodwin RG, Smith CA.  
 DR WPI; 92-366255/44.  
 DR N-PSDB; Q29745.  
 PT Isolated viral proteins are cytokine (e.g. TNF) antagonists - for  
 PT regulating immune response and for treating cachexia septic shock  
 PT and side effects associated with cytokine therapy  
 PS Claim 3; Page 28; 39pp; English.  
 CC The sequence is that of myxoma virus T2 protein which acts as a  
 CC TNF antagonist by binding TNF and preventing it from binding to TNF  
 CC receptors. It can be used for regulating immune responses, treating  
 CC cachexia or septic shock or to treat side effects associated with  
 CC cytokine therapy, e.g. TNF anti-tumour therapy. It may also be used  
 CC as an immunogen, a reagent in assays and as a binding agent for  
 CC affinity purifications. See also R27865.  
 SQ Sequence 326 AA;

Query Match         6.6%; Score 180; DB 5; Length 326;  
 Best Local Similarity 34.4%; Pred. No. 8.91e-06;  
 Matches 31; Conservative 20; Mismatches 34; Indels 5; Gaps 4;

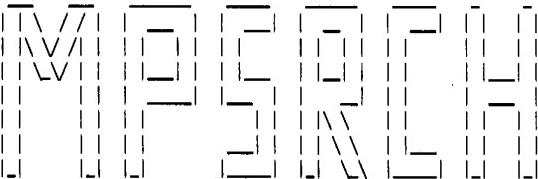
Db 61 cspcknet-ftastnhapacvscrgrctghlsesqscdktrdrvcdcsagnyclkgqeg 119  
   |  |  |  |  |  |  |  |  |  |  |  |  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCCTVC-KSGQTNKSSCTTRDTVCQCEKGSFQDKNSPEM 154  
 Db 120 cricapktkcpagyg-vsghtrtgvdvlctk 148  
   |  |  |  |  |  |  |  |  |  |:  
 Qy 155 CRTC--RTGCPGRGMVKVSNCPRSDIKCKN 182

RESULT 15  
 ID R85072 standard; Protein; 326 AA.  
 AC R85072;  
 DT 16-APR-1996 (first entry)  
 DE Myxoma virus T2 protein.  
 KW Myxoma virus; immunosuppressive; cytokine antagonist;  
 KW tumour necrosis factor antagonist; therapeutic; cachexia;  
 KW septic shock.  
 OS Myxoma virus.  
 PN US5464938-A.  
 PD 07-NOV-1995.  
 PF 18-AUG-1994; 292549.  
 PR 19-OCT-1992; US-963330.  
 PA (IMMV ) Immunex Corp.  
 PI Goodwin RG, Smith CA  
 DR WPI; 95-402861/51.  
 DR N-PSDB; T02471.  
 PT New soluble viral proteins that bind tumour necrosis factor - for  
 PT treating cachexia, septic shock, side effects of TNF therapy etc.,  
 PT also useful in assays, affinity purific. and antibody prodn.  
 PS Claim 1; Columns 31-32; 21pp; English.  
 CC The myxoma virus T2 protein is a soluble viral protein which  
 CC binds tumour necrosis factor (TNF), thus inhibiting TNF binding

CC to its receptor. T2 protein is useful (when administered by  
 CC injection or infusion from sustained release implants, etc.) for  
 CC treating TNF associated toxicity e.g. side effects of using TNF as  
 CC an antitumour agent or in cases of cachexia and septic shock where  
 CC TNF production is excessive.  
 SQ Sequence 326 AA;

Query Match         6.6%; Score 180; DB 15; Length 326;  
 Best Local Similarity 34.4%; Pred. No. 8.91e-06;  
 Matches 31; Conservative 20; Mismatches 34; Indels 5; Gaps 4;  
 Db 61 cspcknet-ftastnhapacvscrgrctghlsesqscdktrdrvcdcsagnyclkgqeg 119  
   |  |  |  |  |  |  |  |  |  |  |  |  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCCTVC-KSGQTNKSSCTTRDTVCQCEKGSFQDKNSPEM 154  
 Db 120 cricapktkcpagyg-vsghtrtgvdvlctk 148  
   |  |  |  |  |  |  |  |  |  |:  
 Qy 155 CRTC--RTGCPGRGMVKVSNCPRSDIKCKN 182

Search completed: Thu May 14 16:50:59 1998  
 Job time : 49 secs.

\*\*\*\*\*  
  
 \*\*\*\*\*  
 (TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 14 16:49:23 1998; MasPar time 16.85 Seconds  
 836.713 Million cell updates/sec

Tabular output not generated.

Title: >US-08-918-874-1  
 Description: (1-386) from US08918874.pep  
 Perfect Score: 2715  
 Sequence: 1 MGLNGQSVPTASSARAGRYP.....VGSEKLFYEEDEAGSATSC 386

Scoring table: PAM 150  
 Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: pir56  
 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 46.756; Variance 102.161; scale 0.458

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query						
No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	191	7.0	335	2	A40036	apoptosis-mediating s	8.42e-13
2	191	7.0	459	2	I48854	gene murine tumour ne	8.42e-13
3	189	7.0	474	2	B38634	tumor necrosis factor	1.70e-12
4	187	6.9	349	2	D36858	gene G4R protein - va	3.43e-12
5	185	6.8	427	1	GQHUN	nerve growth factor r	6.91e-12
6	184	6.8	461	2	JCA302	tumor necrosis factor	9.79e-12
7	182	6.7	314	2	I37383	FAS soluble protein -	1.96e-11
8	180	6.6	326	1	GQVZML	T2 protein - myxoma v	3.93e-11
9	176	6.5	324	2	JC2395	Fas antigen - rat	1.56e-10
10	177	6.5	327	2	A46484	apoptosis-mediating m	1.11e-10
11	173	6.4	139	5	ITNRR	tumor necrosis factor	4.36e-10
12	173	6.4	140	5	1NCFA	tumor necrosis factor	4.36e-10
13	173	6.4	142	5	1NCFB	tumor necrosis factor	4.36e-10
14	173	6.4	158	5	IEXTB	tumor necrosis factor	4.36e-10
15	173	6.4	160	5	IEXTA	tumor necrosis factor	4.36e-10
16	173	6.4	455	1	GQHUT1	tumor necrosis factor	4.36e-10
17	170	6.3	416	2	JN0006	nerve growth factor r	1.21e-09
18	171	6.3	425	2	A26431	nerve growth factor r	8.63e-10
19	166	6.1	325	2	B43692	T2 protein - rabbit f	4.69e-09
20	159	5.9	461	1	GQRTT1	tumor necrosis factor	4.87e-08
21	158	5.8	461	2	A35356	tumor necrosis factor	6.79e-08
22	156	5.7	454	1	GQMST1	tumor necrosis factor	1.31e-07
23	156	5.7	454	2	I57826	tumor necrosis factor	1.31e-07

24	151	5.6	271	2	S12783	OX40 antigen precursor	6.75e-07
25	151	5.6	272	2	I48700	gene ox40 protein - m	6.75e-07
26	144	5.3	256	2	B32393	T-cell antigen 4-1BB	6.43e-06
27	144	5.3	435	2	I54182	tumor necrosis factor	6.43e-06
28	137	5.0	255	2	JT0752	lymphocyte activation	5.86e-05
29	134	4.9	260	1	A46517	CD27 antigen precursor	1.49e-04
30	127	4.7	493	2	JC5486	membrane glycoprotein	1.26e-03
31	125	4.6	595	2	A42086	CD30 antigen precursor	2.29e-03
32	118	4.3	250	1	A49053	CD27 antigen precursor	1.80e-02
33	111	4.1	183	2	S52904	virion protein j13L -	1.32e-01
34	111	4.1	185	2	S52903	virion protein j13L -	1.32e-01
35	110	4.1	277	2	A60771	B-cell activation pro	1.74e-01
36	110	4.1	512	2	I80311	sepC protein - Escher	1.74e-01
37	108	4.0	85	2	I55492	myosin heavy chain -	3.02e-01
38	109	4.0	176	2	S52914	virion protein j13L -	2.29e-01
39	109	4.0	189	2	S52907	virion protein j13L -	2.29e-01
40	109	4.0	191	2	S52905	virion protein j13L -	2.29e-01
41	109	4.0	420	2	B38104	LFY floral meristem i	2.29e-01
42	109	4.0	1790	1	MMFPB1	laminin chain B1 prec	2.29e-01
43	108	4.0	3133	2	S52093	hemocytin - silkworm	3.02e-01
44	105	3.9	189	2	S52902	virion protein j13L -	6.84e-01
45	104	3.8	431	1	BWBSSY	preprotein translocas	8.95e-01

#### ALIGNMENTS

RESULT	1
ENTRY	A40036 #type complete
TITLE	apoptosis-mediating surface antigen Fas precursor - humanALTERNATE_N
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 10-Sep-1997
ACCESSIONS	A40036; S24543; A38142
REFERENCE	A40036
#authors	Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Samematsu, M.; Hase, A.; Seto, Y.; Nagata, S.
#journal	Cell (1991) 66:233-243
#title	The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis.
#cross-references	MUID:91309137
#accession	A40036
#status	preliminary
#molecule_type	mRNA
#residues	1-335 ##label ITO
#cross-references	GB:M67454; NID:g182409; PID:g182410
REFERENCE	S24543
#authors	Krammer, P.H.
#submission	submitted to the EMBL Data Library, February 1992
#accession	S24543
#status	preliminary
#molecule_type	mRNA
#residues	1-335 ##label KRA
#cross-references	EMBL:X63717; NID:g28741; PID:g28742
REFERENCE	A38142
#authors	Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Richards, S.; Dhein, J.; Trauth, B.C.; Ponsting, H.; Krammer, P.H.
#journal	J. Biol. Chem. (1992) 267:10709-10715
#title	Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas antigen.
#cross-references	MUID:92268122
#accession	A38142
#status	preliminary; not compared with conceptual translation
#molecule_type	nucleic acid
#residues	1-134,'1',136-335 ##label OEH
#experimental_source	SKW6.4 cells
#note	sequence extracted from NCBI backbone (NCBIP:103810)
#note	in NCBI backbone the source is designated as mouse
GENETICS	
#gene	GDB:AP1

##cross-references GDB:132671; OMIM:134637  
 #map\_position 10q4.1-10q4.1  
 CLASSIFICATION #superfamily NGF receptor repeat homology  
 KEYWORDS apoptosis; surface antigen; transmembrane protein  
 FEATURE  
 1-16 #domain signal sequence #status predicted #label SIG\  
 85-128 #domain NGF receptor repeat homology #label NG4\  
 174-190 #domain transmembrane #status predicted #label TMM  
 SUMMARY #length 335 #molecular\_weight 37732 #checksum 4899

Query Match 7.0t; Score 191; DB 2; Length 335;  
 Best Local Similarity 35.1t; Pred. No. 8.42e-13;  
 Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;

Db 82 CVPCQEGKEYTDKAHFSSKCRRCRLDEGHGLEVEINCRTNTKCRCKPNFCNSTVCE 141  
 ||| ||::|| :: :| |::| :| :| :|||::|:| | :|  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCVCKSGQT-N-KSSCTTTRDTVCQCCKGSFQDKNSPE 153  
 Db 142 HCDPC-TKCEHGLIK--ECLTLSNTKCKEEGSRSNLG 175  
 ||| ||::|:|| ::|| |:| ||::|:|| |:  
 Qy 154 MCRTCRTGCPGMVKVSNCPRSDIKCKNESAASTG 190

RESULT 2  
 ENTRY I48854 #type fragment

TITLE gene murine tumour necrosis factor receptor 2 protein - mouse  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change  
 23-Feb-1997

ACCESSIONS I48854  
 REFERENCE I48854  
 #authors Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
 #journal Mamm. Genome (1994) 5:726-727  
 #title Allelic variation of the type 2 tumor necrosis factor  
 receptor gene.  
 #cross-references MUID:95178848

#accession I48854  
 ##status preliminary; translated from GB/EMBL/DDBJ  
 ##molecule\_type mRNA  
 ##residues 1-459 ##label RES

##cross-references EMBL:X76401; NID:g433830; PID:g433831

CLASSIFICATION #superfamily tumor necrosis factor receptor type 2; NGF  
 receptor repeat homology  
 SUMMARY #length 459 #checksum 3156

Query Match 7.0t; Score 191; DB 2; Length 459;  
 Best Local Similarity 27.6t; Pred. No. 1.70e-12;  
 Matches 29; Conservative 27; Mismatches 44; Indels 5; Gaps 5;

Db 61 CADCEASM-YTQVWNQFRCLSCSSCSTDQVETRACTKQQNRCVACEAGRYCALKTHSG 119  
 ||| ::|| |:|::|:|:|:|:|:|:|:|:|:  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCV-CKSGQTNKSSCTTTRDTVCQCCKGSFQD-KNSPE 153

Db 120 SCRQCMLRSKCGPGFGVASSRAPNGNVLKACAPGTFSDTTSSTD 164  
 ||| |:| | |:|:|:|:|:|:|:|:  
 Qy 154 MCRTC-RTG-CPRGMVKVSNCPRSDIKCKNESAASTGKTPAAE 196

RESULT 3  
 ENTRY B38634 #type complete

TITLE tumor necrosis factor receptor type 2 precursor - mouse  
 ORGANISM  
 DATE 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change  
 08-Sep-1997

ACCESSIONS B38634; A40254; S54816  
 REFERENCE A38634  
 #authors Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,  
 G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.  
 #journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834  
 #title Cloning and expression of cDNAs for two distinct murine tumor  
 necrosis factor receptors demonstrate one receptor is  
 species specific.

##cross-references MUID:91187885  
 #accession B38634  
 ##molecule\_type mRNA  
 ##residues 1-474 ##label LEW  
 ##cross-references GB:M60469; NID:g199827; PID:g199828  
 REFERENCE A40254  
 #authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,  
 C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.  
 #journal Mol. Cell. Biol. (1991) 11:3020-3026  
 #title Molecular cloning and expression of the type 1 and type 2  
 murine receptors for tumor necrosis factor.

##cross-references MUID:91246168  
 #accession A40254  
 ##molecule\_type mRNA  
 ##residues 1-474 ##label GOO  
 ##cross-references GB:M60469; NID:g199827; PID:g199828  
 REFERENCE S54816  
 #authors Kissonherghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky,  
 Y.  
 #submission submitted to the EMBL Data Library, May 1995  
 #description Characterization of the promoter region of the murine p75-TNF  
 receptor.

#accession S54816  
 ##status preliminary  
 ##molecule\_type DNA  
 ##residues 1-22 ##label KIS  
 ##cross-references EMBL:X87128; NID:g809043; PID:g809044  
 CLASSIFICATION #superfamily tumor necrosis factor receptor type 2; NGF  
 receptor repeat homology  
 KEYWORDS cytokine receptor; transmembrane protein  
 FEATURE  
 1-22 #domain signal sequence #status predicted #label SIG\  
 23-474 #product tumor necrosis factor receptor type 2 #status  
 predicted #label MAT\  
 40-77 #domain NGF receptor repeat homology #label NC1\  
 79-120 #domain NGF receptor repeat homology #label NC2\  
 166-203 #domain NGF receptor repeat homology #label NG4  
 SUMMARY #length 474 #molecular\_weight 50319 #checksum 7767

Query Match 7.0t; Score 189; DB 2; Length 474;  
 Best Local Similarity 27.6t; Pred. No. 1.70e-12;  
 Matches 29; Conservative 27; Mismatches 44; Indels 5; Gaps 5;

Db 76 CADCEASM-YTQVWNQFRCLSCSSCTTDQVETRACTKQQNRCVACEAGRYCALKTHSG 134  
 ||| ::|| |:|::|:|:|:|:|:|:  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCV-CKSGQTNKSSCTTTRDTVCQCCKGSFQD-KNSPE 153

Db 135 SCRQCMLRSKCGPGFGVASSRAPNGNVLKACAPGTFSDTTSSTD 179  
 ||| |:| | |:|:|:|:|:|:  
 Qy 154 MCRTC-RTG-CPRGMVKVSNCPRSDIKCKNESAASTGKTPAAE 196

RESULT 4  
 ENTRY D36858 #type complete

TITLE gene G4R protein - variola virus ALTERNATE NAMES B28R protein (COP)  
 ORGANISM #formal\_name variola virus  
 DATE 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change  
 10-Sep-1997

ACCESSIONS D36858; S46888; S32385; S35987  
 REFERENCE A36859  
 #authors Blinov, V.M.  
 #submission submitted to GenBank, November 1992  
 #description not shown.  
 #accession D36858  
 ##status preliminary  
 ##molecule\_type DNA  
 ##residues 1-349 ##label BLI  
 ##cross-references GB:X69198; NID:g456758; PID:g457087  
 ##experimental\_source strain India-1967, ssp. major, isolate Ind3  
 REFERENCE S46868  
 #authors Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov,  
 S.G.; Chizhikov, V.E.; Frolov, I.V.; Totmenin, A.V.-

Shchelkunov, S.N.; Sandakhchiev, L.S.  
 #submission submitted to the EMBL Data Library, April 1992  
 #description Nucleotide sequence analysis of the region of variola virus  
     XhoI F O H P Q genome fragment.  
 #accession S46888  
     ##status preliminary  
     ##molecule\_type DNA  
     ##residues 1-349 ##label KOL  
     ##cross-references EMBL:X67117; NID:g516428; PID:g516449  
     ##experimental\_source strain India-1967, isolate Ind3  
 REFERENCE S32385  
     #authors Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.  
     #journal FEBS Lett. (1993) 319:80-83  
     #title Genes of variola and vaccinia viruses necessary to overcome  
         the host protective mechanisms.  
 #accession S32385  
     ##molecule\_type DNA  
     ##residues 31-168 ##label SHC  
     ##cross-references EMBL:X69198  
     ##experimental\_source strain India-1967, ssp. major  
 GENETICS  
     #gene G4R  
 CLASSIFICATION \*superfamily NGF receptor repeat homology  
 FEATURE  
     68-109           #domain NGF receptor repeat homology #label NG2\  
     110-151           #domain NGF receptor repeat homology #label NG3  
 SUMMARY        #length 349 #molecular-weight 38189 #checksum 2016  
 Query Match        6.9%; Score 187; DB 2; Length 349;  
 Best Local Similarity 37.1%; Pred. No. 3.43e-12;  
 Matches 33; Conservative 18; Mismatches 31; Indels 7; Gaps 6;  
 Db        65 CTPCGSGT-FTSRNNHLPACLSCNCNSNQVETRSCNTTHNRICECSPGYYCLLGSSG 123  
     | || | : | : ||::|| | | : || ||:: || | : || : ||:  
 Qy        96 CNPCTEGVDYTIASSNLPSCLLCTV-CKSGQTNKSSCTTRDTVCQCEKGSF-QDKNSPE 153  
 Db        124 -CKACVSQTAKCGIGYG-VSGHTSVGDVIC 150  
     |::| :|| | || | : || : ::|:  
 Qy        154 MCRTC--RTGCPRGMVKSNCPTPRSDIKC 180  
 RESULT        5  
 ENTRY        GQHUN        #type complete  
 TITLE        nerve growth factor receptor precursor, low affinity - human ALTERNATE\_N  
 ORGANISM     #formal\_name Homo sapiens #common\_name man  
 DATE        31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change  
     20-Mar-1998  
 ACCESSIONS    A25218; A60204; S21689; I57638  
 REFERENCE     A25218  
     #authors Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.;  
         Mercer, E.; Bothwell, M.; Chao, M.  
     #journal Cell (1986) 47:545-554  
     #title Expression and structure of the human NGF receptor.  
     ##cross-references MUID:87051725  
 #accession     A25218  
     ##molecule\_type mRNA  
     ##residues 1-427 ##label JOH  
     ##cross-references GB: M14764; NID:g189204; PID:g189205  
 REFERENCE     A60204  
     #authors Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman,  
         G.; Thompson, S.; Grob, P.; Ross, A.H.; Bothwell, M.;  
         Atkinson, B.F.; Koprowski, H.  
     #journal J. Neurochem. (1987) 48:225-232  
     #title Purification and amino terminal sequencing of human melanoma  
         nerve growth factor receptor.  
     ##cross-references MUID:87085574  
 #accession     A60204  
     ##molecule\_type protein  
     ##residues 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 ##label  
         MAR  
     ##experimental\_source melanoma cell line A875  
     ##note this sequence has been corrected by a note added in

proof to follow the nucleotide translation from a published report

**REFERENCE** S21689  
**#authors** Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.  
**#journal** Arch. Biochem. Biophys. (1992) 294:244-252  
**#title** Structural domains of the extracellular domain of human nerve growth factor receptor detected by partial proteolysis.  
**#cross-references** MUID:92198017  
**#accession** S21689  
**##status** preliminary  
**##molecule\_type** protein  
**##residues** 183-208 ##label VIS  
**REFERENCE** I57638  
**#authors** Sehgal, A.; Patil, N.; Chao, M.  
**#journal** Mol. Cell. Biol. (1988) 8:3160-3167  
**#title** A constitutive promoter directs expression of the nerve growth factor receptor gene.  
**#cross-references** MUID:89096903  
**#accession** I57638  
**##status** preliminary; translated from GB/EMBL/DDJB  
**##molecule\_type** DNA  
**##residues** 1-22 ##label RES  
**##cross-references** GB:M21621; NID:g189206; PID:g189207  
**COMMENT** This receptor is found on sensory and sympathetic neurons; on neuroblastoma cells, and on a variety of nonneuronal derivatives of the neural crest.  
**COMMENT** The cysteine-rich region of the extracellular domain may form part or all of the NGF-binding site.  
**COMMENT** This protein is thought to form a high-affinity receptor when it associates with the 140K trk proto-oncogene, which contains an intracellular tyrosine kinase domain.  
**COMMENT** This receptor undergoes both N- and O-linked glycosylation.  
**GENETICS**  
**#gene** GDB:NGFR  
**#cross-references** GDB:120234; OMIM:162010  
**#map\_position** 17q21-17q22  
**CLASSIFICATION** #superfamily nerve growth factor receptor; NGF receptor repeat homology  
**KEYWORDS** duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; transmembrane protein  
**FEATURE**  
1-28                    #domain signal sequence #status predicted #label SIG\  
29-427                #product nerve growth factor receptor #status  
                          experimental #label MAT\  
29-250                #domain extracellular #status predicted #label EXT\  
29-190                #region cysteine-rich\  
32-65                 #domain NGF receptor repeat homology #label NG1\  
67-108                #domain NGF receptor repeat homology #label NG2\  
109-147               #domain NGF receptor repeat homology #label NG3\  
149-189               #domain NGF receptor repeat homology #label NG4\  
197-248               #region serine/threonine-rich\  
251-272               #domain transmembrane #status predicted #label TRM\  
273-427               #domain intracellular #status predicted #label INT\  
60                      #binding\_site carbohydrate (Asn) (covalent) #status  
                          predicted  
**SUMMARY**            #length 427 #molecular-weight 45183 #checksum 7426  
  
Query Match            6.8%; Score 185; DB 1; Length 427;  
Best Local Similarity 29.4%; Pred. No. 6.91e-12;  
Matches 25; Conservative 21; Mismatches 37; Indels 2; Gaps 2;  
  
Db        64 CEPCLDSVTFSDVVSSATEPCKPCTECVGLQSMSAPCVEADDAVCRAYYYQD-ETTGRC 122  
          ::|| :: :: : : || | : | : ::| : ||::| | :|| :: |  
Qy        96 CNPCTEGVDITYIASNLPSCLLCTVKCSGQTINKSSCTTTRDTVCQCCEKGSFQDKNSPEMC 155  
  
Db        123 EACRV-CEAGSGLVFSCQDKQNTVC 146  
          ::|| | | | :| : : |  
Qy        156 RTCRTGCPGRMVKSNCPRSDIKC 180  
  
**RESULT** 6  
**ENTRY** JC4302        #type complete

Db 82 CVPCQEGKEYTDKAHFFSKCRCLRCDEGHGLEVEINCTRQNTKCRCKPNFFCNSTVCE 141  
   | || | : | : | | : | : | : | : | : | : |  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCVCKSGQT-N-KSSCTTTRDTVCQCCEKGSFQDKNSPE 153

Db 142 HCDPC-TKCEHGIK--BCTLTSNTKCKEE 168  
   | | | | : | : | : | : | : | : | : |  
 Qy 154 MCRTCRTGCPGMVKVSNCPRSDIKCKNE 183

**RESULT** 8  
**ENTRY** GQVZML #type complete

**TITLE** T2 protein - myxoma virus (strain Lausanne) **ORGANISM** #formal\_name  
**DATE** 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change  
           24-Oct-1997

**ACCESSIONS** A40566  
**REFERENCE** A40566  
 #authors Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.  
 #journal Virology (1991) 184:370-382  
 #title Myxoma virus expresses a secreted protein with homology to  
       the tumor necrosis factor receptor gene family that  
       contributes to viral virulence.  
 #cross-references MUID:91335768  
 #accession A40566  
 ##molecule\_type DNA  
 ##residues 1-326 ##label UPT  
 ##cross-references GB:M95181; GB:M37976; NID:g332309; PID:g332310  
**CLASSIFICATION** #superfamily myxoma virus T2 protein; NGF receptor repeat  
                  homology  
**KEYWORDS** glycoprotein  
**FEATURE**  
 64-105           #domain NGF receptor repeat homology #label NG2\  
 106-147           #domain NGF receptor repeat homology #label NG3\  
 66,181,205,238   #binding\_site carbohydrate (Asn) (covalent) #status  
                  predicted  
**SUMMARY** #length 326 #molecular-weight 35208 #checksum 9255

Query Match       6.68; Score 180; DB 1; Length 326;  
 Best Local Similarity 34.4%; Pred. No. 3.93e-11;  
 Matches 31; Conservative 20; Mismatches 34; Indels 5; Gaps 4;

Db 61 CSPCKNET-FTASTNHAPACVSCRGRCGTGHLESESQSCDKTRDRVCDCSAGNYCLLKQEG 119  
   | : | : | : | : | : | : | : | : | : | : |  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCV-CKSGQTNKSSCTTTRDTVCQCCEKGSFQDKNSPEM 154

Db 120 CRICAPTKCPAGYG-VSGHTRTGDLCTK 148  
   | | | : | | | | : | : |  
 Qy 155 CRTCA--RTGCPGMVKVSNCPRSDIKCKN 182

**RESULT** 9  
**ENTRY** JC2395 #type complete

**TITLE** Fas antigen - rat **ORGANISM** #formal\_name Rattus norvegicus #co  
**DATE** 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change  
           10-Sep-1997

**ACCESSIONS** JC2395; PC2246  
**REFERENCE** JC2395  
 #authors Kimura, K.; Wakatsuki, T.; Yamamoto, M.  
 #journal Biochem. Biophys. Res. Commun. (1994) 198:666-674  
 #title A variant mRNA species encoding a truncated form of Fas  
       antigen in the rat liver.  
 #accession JC2395  
 ##molecule\_type mRNA  
 ##residues 1-324 ##label KIM  
 ##cross-references DDBJ:D26112; NID:g468486; PID:d1005650; PID:g468487  
 ##experimental\_source thymus  
 #accession PC2246  
 ##molecule\_type mRNA  
 ##residues 1-62, 'RFT' ##label KI2  
 ##cross-references DDBJ:D26113; NID:g468488; PID:d1005651; PID:g468489  
 ##experimental\_source liver

```

GENETICS
#introns      62/1
CLASSIFICATION #superfamily NGF receptor repeat homology
KEYWORDS       transmembrane protein
FEATURE
  1-21          #domain signal sequence #status predicted #label SIG\
  22-324         #product Fas antigen #status predicted #label MAT\
  81-124         #domain NGF receptor repeat homology #label NG4\
  171-188        #domain transmembrane #status predicted #label TMM
SUMMARY        #length 324 #molecular-weight 36835 #checksum 7305

```

Query Match 6.5%; Score 176; DB 2; Length 324;  
Best Local Similarity 31.2%; Pred. No. 1.56e-10;  
Matches 29; Conservative 23; Mismatches 37; Indels 4; Gaps 4;

Db 77 TCHPCTEGEYTYDRKHSYDKCRCAFCDEGHGLEVETNCTRTQNTKCRCKENFYCNASLC 136  
:::||||| :|| : | :| :| :| :| :| :| :| :| :| :|

Db 137 DHCYHC-TSCGLEDI-LEPCTRTSNTKCKKQSS 167

Ov. 153 EMCRTGRTGCRGCMVKVSNCTRRSRDIKCKNESA 185

Qy 193 EMERITICRIGCFRGMVRVSNCIPRSDEKANEHA 165

RESULT 10  
ENTRY A46484 #type complete

TITLE apoptosis-mediating membrane-associated polypeptide Fas  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change  
20-Mar-1999

20-May-1996  
ACCESSIONS A46484; A47254  
REFERENCE A46484  
#authors Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, N.A.; Nagata, S.  
#journal J. Immunol. (1992) 148:1274-1279  
#title The cDNA structure, expression, and chromosomal assignment of the mouse Fas antigen.  
#cross-references MUID:92148151  
#accession A46484  
##status preliminary  
##molecule\_type mRNA  
##residues 1-327 ##label WAT  
##cross-references GB:M83649; NID:g193225; PID:g193226  
##experimental\_source BAM3 macrophage cell line  
##note sequence extracted from NCBI backbone (NCBIN:81544, NCBIPI:81545)

REFERENCE A47254  
#authors Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1756-1760  
#title Aberrant transcription caused by the insertion of an early transposable element in an intron of the Fas antigen gene of lpr mice.

#cross-references MUID:93189576

```
#accession A47254
##status preliminary
##molecule_type nucleic acid
##residues 1-96 ##label ADA
##experimental_source MRL lpr/lpr
##note sequence extracted from NCBI backbone (NCBIN:126850,
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CLASSIFICATION #superfamily NGF receptor repeat homology  
KEYWORDS transmembrane protein

**KEYWORDS** transmembrane protein  
**FEATURE**

81-124 #domain NGE rece

SUMMARY #length 327 #molecular-weight 37417 #checksum 8479

Query Match 6.5%; Score 177; DB 2; Length 327;  
Best Local Similarity 30.5%; Pred. No. 1.11e-10;  
Matches 29; Conservative 25; Mismatches 36; Indels 5; Gaps 5;

Db 75 TPTCAPTEGKEYMDKNHYADKCCRRTLCDEEHGLEVETNCTLTQNCKCKPDFYCDSP 134  
| : | |||| :| :: | ||:| : : ::| ||::| | :|

Qy 93 TGACNPCTEGVDYTIASNNLPSCLLCVCKSGQT-N-KSCTTTRDTCQCCEKGSFQDKN 150  
Db 135 GCBHCVRC-ASCEHGTLE-P-CTATSNTNCRKQSP 166  
: | : | ::| :| : : ||| :| :| :||:|:  
Qy 151 SPEMCRTCRTGCPGRMVKVSNTTPRSIDKCKNES 185

RESULT 11  
ENTRY 1TNRR #type complete

**TITLE** tumor necrosis factor receptor type 1 (P55 extracellular  
**ORGANISM** #formal\_name Homo sapiens #common\_name man  
**#note** recombinant form expressed in Baculovirus SF9  
**REFERENCE** A52442  
**#authors** Banner, D.W.  
**#submission** submitted to the Brookhaven Protein Data Bank, May 1994  
**#cross-references** PDB:1TNR  
**REFERENCE** A40737  
**#authors** Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
                   H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
**#journal** Cell (1993) 73:431-445  
**#title** Crystal structure of the soluble human 55 kd TNF  
                   receptor-human TNF $\beta$  complex: implications for TNF  
                   receptor activation.  
**REFERENCE** TN034093  
**#authors** D'Arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;  
                   Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;  
                   Lesslauer, W.  
**#journal** J. Mol. Biol. (1993) 229:555  
**#title** Crystallization and preliminary analysis of tnf-beta and a  
                   tnf-beta:55 kd tnf receptor complex.

```

COMMENT Resolution: 2.85 angstroms
COMMENT Determination: X-ray diffraction
KEYWORDS Complex(lymphokineRECEPTOR)
FEATURE
  1-15      #disulfide_bonds\
  16-29     #disulfide_bonds\
  19-38     #disulfide_bonds\
  41-56     #disulfide_bonds\
  59-74     #disulfide_bonds\
  62-82     #disulfide_bonds\
  84-100    #disulfide_bonds\
  103-115   #disulfide_bonds\
  106-123   #disulfide_bonds\
  125-136   #disulfide_bonds
SUMMARY      #length 139 #molecular-weight 15746 #checksum 5235

```

Query Match 6.4%; Score 173; DB 5; Length 139;  
Best Local Similarity 37.1%; Pred. No. 4.36e-10;  
Matches 33; Conservative 12; Mismatches 37; Indels 7; Gaps 6;

Db 38 CRECESG-SFTASENHLRHLCSCSKRKEMGQVEISSCTVDRDTCVGCRKNQYRHYWSEN 96  
| | | : | : | : | | : | | : | ||| | | | | : | : |  
Qy 96 CNPCTEGVDYTIASNNPLSCLLCTVC-KS-GQTINNKSSCTTTRDTCVQCCKGSFQDKNSPE 153

Db 97 LFQCFNCSL-CLNGTVHLS-CQEKGNTVC 123  
: | | | | | :| | : : |

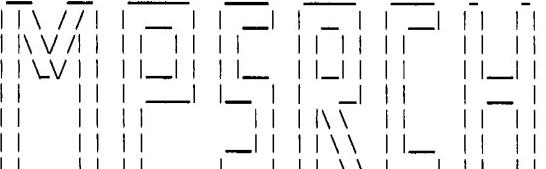
RESULT 12  
ENTRY 1NCFA #type complete

**TITLE** tumor necrosis factor receptor 55 kd extracellular domain  
contains residues 12-172 of the mature receptor sequence,  
chain A - hu

**ALTERNATE\_NAMES** stnfr1; type i receptor  
**ORGANISM** #formal\_name Homo sapiens #common\_name man  
**#note** expressed in Escherichia coli, residue 11 is mutated to met  
 as a result of the expression system  
**REFERENCE** A66195  
**#authors** Naismith, J.H.; Sprang, S.R.  
**#submission** submitted to the Brookhaven Protein Data Bank, October 1994





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 (TM)  
 \*\*\*\*\*

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 14 16:47:33 1998; MasPar time 11.24 Seconds  
 861.719 Million cell updates/sec

Tabular output not generated.

Title: >US-08-918-874-1  
 Description: (1-386) from US08918874.pep  
 Perfect Score: 2715  
 Sequence: 1 MCLWGQSVPTASSARAGRYP.....VGSEKLFYEEDEAGSATSC 386

Scoring table: PAM 150  
 Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot35  
 1:swiss1

Statistics: Mean 48.960; Variance 85.763; scale 0.571

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	216	8.0	323	1	FASA_BOVIN	FASL RECEPTOR PRECURSO	6.03e-21		
2	191	7.0	335	1	FASA_HUMAN	FASL RECEPTOR PRECURSO	3.59e-16		
3	189	7.0	474	1	TNRC_MOUSE	TUMOR NECROSIS FACTOR	8.49e-16		
4	187	6.9	349	1	VC22_VARV	PROTEIN C22/B28 HOMOLO	2.00e-15		
5	185	6.8	427	1	NGFR_HUMAN	LOW-AFFINITY NERVE GRO	4.71e-15		
6	184	6.8	451	1	TNRL_PIG	TUMOR NECROSIS FACTOR	7.22e-15		
7	180	6.6	326	1	VIT2_MYXVL	TUMOR NECROSIS FACTOR	3.95e-14		
8	177	6.5	327	1	FASA_MOUSE	FASL RECEPTOR PRECURSO	1.40e-13		
9	173	6.4	455	1	TNRL_HUMAN	TUMOR NECROSIS FACTOR	7.47e-13		
10	170	6.3	416	1	NGFR_CHICK	LOW-AFFINITY NERVE GRO	2.60e-12		
11	171	6.3	425	1	NGFR_RAT	LOW-AFFINITY NERVE GRO	1.72e-12		
12	166	6.1	325	1	VIT2_SFVKA	TUMOR NECROSIS FACTOR	1.36e-11		
13	159	5.9	461	1	TNRL_RAT	TUMOR NECROSIS FACTOR	2.35e-10		
14	158	5.8	461	1	TNRC_HUMAN	TUMOR NECROSIS FACTOR	3.51e-10		
15	156	5.7	454	1	TNRL_MOUSE	TUMOR NECROSIS FACTOR	7.85e-10		
16	151	5.6	271	1	OX40_RAT	OX40L RECEPTOR PRECURS	5.75e-09		
17	151	5.6	272	1	OX40_MOUSE	OX40L RECEPTOR PRECURS	5.75e-09		
18	144	5.3	256	1	41BB_MOUSE	4-1BB LIGAND RECEPTOR	8.88e-08		
19	144	5.3	435	1	TNRC_HUMAN	LYMPHOTOXIN-BETA RECEP	8.88e-08		
20	132	4.9	255	1	41BB_HUMAN	4-1BB LIGAND RECEPTOR	8.39e-06		
21	131	4.8	260	1	CD27_HUMAN	CD27L RECEPTOR PRECURS	1.21e-05		
22	130	4.8	277	1	OX40_HUMAN	OX40L RECEPTOR PRECURS	1.76e-05		
23	125	4.6	595	1	CD30_HUMAN	CD30L RECEPTOR PRECURS	1.08e-04		

24	125	4.6	719	1	YMP8_CAEEL	HYPOTHETICAL	82.6 KD P	1.08e-04
25	118	4.3	250	1	CD27_MOUSE	CD27L RECEPTOR PRECURS	1.29e-03	
26	113	4.2	415	1	TNRC_MOUSE	LYMPHOTOXIN-BETA RECEP	7.17e-03	
27	110	4.1	277	1	CD40_HUMAN	CD40L RECEPTOR PRECURS	1.96e-02	
28	109	4.0	1789	1	LMB1_DROME	LAMININ BETA-1 CHAIN P	2.73e-02	
29	108	4.0	3133	1	HMCT_BOMMO	HEMOCYTIN PRECURSOR (H	3.79e-02	
30	102	3.8	415	1	BOPH_BRAOL	PUTATIVE TRANSCRIPTION	2.60e-01	
31	104	3.8	431	1	SECY_BACSU	PREPROTEIN TRANSLOCASE	1.38e-01	
32	104	3.8	569	1	HXT8_YEAST	HEXOSE TRANSPORTER HXT	1.38e-01	
33	100	3.7	131	1	NU3M_CANPA	NADH-UBIQUINONE OXIDOR	4.86e-01	
34	101	3.7	424	1	LEAF_ARATH	LEAFY PROTEIN.	3.56e-01	
35	101	3.7	502	1	K2M3_SHEEP	KERATIN, TYPE II MICRO	3.56e-01	
36	100	3.7	549	1	COX1_TRYBB	CYTOCHROME C OXIDASE P	4.86e-01	
37	100	3.7	628	1	RA21_SCHPO	DOUBLE-STRAND-BREAK RE	4.86e-01	
38	98	3.6	85	1	OE18_NPVOP	OCLUSION-DERIVED VIRU	8.98e-01	
39	99	3.6	269	1	CD40_BOVIN	CD40L RECEPTOR PRECURS	6.61e-01	
40	98	3.6	576	1	HXT4_YEAST	LOW-AFFINITY GLUCOSE T	8.98e-01	
41	98	3.6	854	1	UBPN_HUMAN	UBIQUITIN CARBOXYL-TER	8.98e-01	
42	99	3.6	974	1	MYSB_MESAU	MYOSIN HEAVY CHAIN, CA	6.61e-01	
43	98	3.6	1375	1	YIP9_YEAST	HYPOTHETICAL 156.9 KD	8.98e-01	
44	99	3.6	1935	1	MYSB_RAT	MYOSIN HEAVY CHAIN, CA	6.61e-01	
45	99	3.6	1935	1	MYSB_HUMAN	MYOSIN HEAVY CHAIN, CA	6.61e-01	

#### ALIGNMENTS

RESULT 1  
 ID FASA\_BOVIN STANDARD; PRT; 323 AA.  
 AC P51867;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)  
 DE (APO-1 ANTIGEN) (CD95).  
 GN APT1 OR FAS.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; ARTIODACTyla.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 96226401.  
 RA YOO J., STONE R.T., BEATTIE C.W.;  
 RL DNA CELL BIOL. 15:227-234(1996).  
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH- INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS- MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; U34794; G1262193; -.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 323 FASL RECEPTOR.  
 FT DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 171 188 POTENTIAL.  
 FT DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 45 163 3 X TNFR-CYS.  
 FT REPEAT 45 80 TNFR-CYS 1.  
 FT REPEAT 81 124 TNFR-CYS 2.  
 FT REPEAT 125 163 TNFR-CYS 3.  
 FT DOMAIN 238 306 DEATH DOMAIN.  
 SQ SEQUENCE 323 AA; 36445 MW; DA5A2A59 CRC32;

Query Match 8.0%; Score 216; DB 1; Length 323;  
 Best Local Similarity 32.0%; Pred. No. 6.03e-21;  
 Matches 33; Conservative 24; Mismatches 41; Indels 5; Gaps 5;

Db 72 RDGDTPECVLCSEGNEYTDKSHHSDKCIRCSICDEEHGLEVEQNCTRTRNTKCRCKSNFF 131  
 | | | | :|| :|| :: | :|| :| : : :|| || :| :| |

Qy 89 RSEITGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQT-N-KSSCTTTRDTCQCCEKGSF 146

Db 132 CNSSPCEHCNPC-TTCEHG-I-IEKCTPTSNTCKGSRSHANS 171  
 : :: | | | | :| : : :|| :| | | :| :

Qy 147 QDKNSPEMCRTRGCPGRMVKSNCPTPRSDIKCKNESAASST 189

## RESULT 2

ID FASA\_HUMAN STANDARD; PRT; 335 AA.  
 AC P25445;  
 DT 01-MAY-1992 (REL. 22, CREATED)  
 DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)  
 DE (APO-1 ANTIGEN) (CD95 ANTIGEN).  
 GN APT1 OR FAS.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 91309137.

RA ITOH N., YONEHARA S., ISHII A., YONEHARA M., MIZUSHIMA S.I.,

RA SAMESHIMA M., HASE A., SETO Y., NAGATA S.;

RL CELL 66:233-243(1991).

RN [2]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 226-240; 269-291 AND 321-335.

RX MEDLINE; 92268122.

RA OEHM A., BEHRMANN I., FALK W., PAWLITA M., MAIER G., KLAS C.,

RA LI-WEBER M., RICHARDS S., DHEIN J., TRAUTH B.C., PONSTINGL H.,

RA KRAMMER P.H.;

RL J. BIOL. CHEM. 267:10709-10715(1992).

RN [3]

RP STRUCTURE BY NMR OF 218-335.

RX MEDLINE; 97122332.

RA HUANG B., EBERSTADT M., OLEJNICZAK E.T., MEADOWS R.P., FESIK S.W.;

RL NATURE 384:638-641(1996).

CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH- INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS- MEDiated APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;

CC WWW="<http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm>".

DR EMBL; M67454; G182410; -.

DR EMBL; X63717; G28742; -.

DR PIR; A40036; A40036.

DR PIR; S24543; S24543.

DR PDB; 1DDE; 12-NOV-97.

DR MIM; 134637; -.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.

DR PROSITE; PS50017; DEATH\_DOMAIN; 1.

KW APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL;

KW 3D-STRUCTURE.

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 335 FASL RECEPTOR.

FT DOMAIN 17 173 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 174 190 POTENTIAL.

FT DOMAIN 191 335 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 47 166 3 X TNFR-CYS.  
 FT REPEAT 47 83 TNFR-CYS 1.  
 FT REPEAT 84 127 TNFR-CYS 2.  
 FT REPEAT 128 166 TNFR-CYS 3.  
 FT DOMAIN 230 314 DEATH DOMAIN.  
 FT CARBOHYD 118 118 POTENTIAL.  
 FT CARBOHYD 136 136 POTENTIAL.  
 SQ SEQUENCE 335 AA; 37732 MW; 3BF8F973 CRC32;

Query Match 7.0%; Score 191; DB 1; Length 335;  
 Best Local Similarity 35.1%; Pred. No. 3.59e-16;  
 Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;

Db 82 CVPQEQEGKEYTDKAHFSKCRRCRLCDEGHGLEVEINCRTQNTKCRCKPNPFNCNSTVCB 141  
 | | | | :|| :: : | | :| : : | :|| :|| :| :| :

Qy 96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGQT-N-KSSCTTTRDTCQCCEKGSFQDKNSPE 153

Db 142 HCDPC-TKCEHGIK--ECLTSNTKCKEEGSRSNLG 175  
 | | | | :|| :|| :| :|| :|| :| :

Qy 154 MCRTCRTGCPGRMVKSNCPTPRSDIKCKNESAASSTG 190

## RESULT 3

ID TNR2\_MOUSE STANDARD; PRT; 474 AA.  
 AC P25119;

DT 01-MAY-1992 (REL. 22, CREATED)

DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).

GN TNFR2 OR TNFR-2.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 91187885.

RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,

RA WONG G.H., CHEN E.Y., GOEDDEL D.V.;

RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE; 91246168.

RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,

RA COPELAND N.G., JENKINS N.A., SMITH C.A.;

RL MOL. CELL. BIOL. 11:3020-3026(1991).

RN [3]

RP SEQUENCE OF 1-26 FROM N.A.

RC STRAIN=NOD;

RA JACOB C.O., LIU J.;

RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

DR EMBL; M60469; G199828; -.

DR EMBL; M59378; G202095; -.

DR EMBL; U39488; G1145885; -.

DR PIR; B38634; B38634.

DR HSSP; P19438; 1TNR.

DR MGD; MGI-98782; TNFR2.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.

KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.

FT SIGNAL 1 22

FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.

FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 259 288 POTENTIAL.

FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 39 203 4 X TNFR-CYS.

FT REPEAT 39 77 TNFR-CYS 1.

FT REPEAT 78 119 TNFR-CYS 2.

FT REPEAT 120 164 TNFR-CYS 3.

FT REPEAT 165 203 TNFR-CYS 4.

FT DISULFID 40 54 BY SIMILARITY.  
 FT DISULFID 55 68 BY SIMILARITY.  
 FT DISULFID 58 76 BY SIMILARITY.  
 FT DISULFID 79 94 BY SIMILARITY.  
 FT DISULFID 97 111 BY SIMILARITY.  
 FT DISULFID 101 119 BY SIMILARITY.  
 FT DISULFID 121 127 BY SIMILARITY.  
 FT DISULFID 136 145 BY SIMILARITY.  
 FT DISULFID 139 163 BY SIMILARITY.  
 FT DISULFID 166 181 BY SIMILARITY.  
 FT CARBOHYD 69 69 POTENTIAL.  
 FT CARBOHYD 195 195 POTENTIAL.  
 SQ SEQUENCE 474 AA; 50319 MW; DC32B2B6 CRC32;

Query Match 7.0%; Score 189; DB 1; Length 474;  
 Best Local Similarity 27.6%; Pred. No. 8.49e-16;  
 Matches 29; Conservative 27; Mismatches 44; Indels 5; Gaps 5;

Db 76 CADCEASM-YTQVWNQFRCLSCSSCTTDQVEIRACTKQQNRCACEACRYCALKTHSG 134  
 ||| ::||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCTV-CKSGQTNKSSCTTRDTVCQCEKGSFQD-KNSPE 153  
 Db 135 SCRQCMLRSKCGPGFGVASSRAPNGVLCKACAPGTFSDTTSSSTD 179  
 ||| :||| :||| :||| :||| :||| :||| :||| :|||:  
 Qy 154 MCRTC-RTG-CPRGMVKVSNCNTPRSDIKCKNESAASTGKTPAAE 196

RESULT 4  
 ID VC22\_VARV STANDARD; PRT; 349 AA.

AC P34015;  
 DT 01-FEB-1994 (REL. 28, CREATED)  
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)  
 DE PROTEIN C22/B28 HOMOLOG.

GN G4R.  
 OS VARIOLA VIRUS.

OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPHOXVIRINAE;  
 OC ORTHOPHOXVIRUSES.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-INDIA-1967 / ISOLATE IND3;

RX MEDLINE; 93202281.

RA SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;

RL FEBS LETT. 319:80-83(1993).

CC -!- SIMILARITY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.

DR EMBL; X69198; G457087; -.

DR EMBL; X67117; G516449; -.

DR PIR; D36858; D36858.

DR PIR; S35987; S35987.

DR PIR; S46888; S46888.

DR HSSP; P19438; ITNR.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.

KW REPEAT.

FT DOMAIN 31 108 2 X TNFR-CYS.

FT REPEAT 31 66 TNFR-CYS 1.

FT REPEAT 67 108 TNFR-CYS 2.

SQ SEQUENCE 349 AA; 38189 MW; 50D0B435 CRC32;

Query Match 6.9%; Score 187; DB 1; Length 349;  
 Best Local Similarity 37.1%; Pred. No. 2.00e-15;  
 Matches 33; Conservative 18; Mismatches 31; Indels 7; Gaps 6;

Db 65 CTPCGSGT-FTSRNNLPACLSCNCRCSNQVETRSCNTTHNRCICECSPGYCLLKGSSG 123  
 ||| | :| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCTV-CKSGQTNKSSCTTRDTVCQCEKGSF-QDKNSPE 153

Db 124 -CKACVSQTKCGIGYG-VSGHTSGVGDVIC 150  
 ||| :| | | ||| :||| :|

Qy 154 MCRTC--RTGCPGRGMVKVSNCNTPRSDIKC 180

RESULT 5

ID NGFR\_HUMAN STANDARD; PRT; 427 AA.  
 AC P08138;  
 DT 01-AUG-1988 (REL. 08, CREATED)  
 DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
 DE (GP80-LNGFR).  
 GN NGFR.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 87051725.  
 RA JOHNSON D., LANAHAN A., BUCK C.R., SEHGAL A., MORGAN C., MERCER E.,  
 RA BOTHWELL M., CHAO M.;  
 RL CELL 47:545-554(1986).  
 CC -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 CC NT-3, AND NT-4.  
 CC -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE  
 CC BOND FORMATION.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; M14764; G189205; -.  
 DR PIR; A25218; GQHUN.  
 DR HSSP; P19438; ITNR.  
 DR MIM; 162010; -.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;  
 KW PHOSPHORYLATION; SIGNAL.  
 FT SIGNAL 1 28  
 FT CHAIN 29 427 NGF RECEPTOR.  
 FT DOMAIN 29 250 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 251 272 POTENTIAL.  
 FT DOMAIN 273 427 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 31 189 4 X TNFR-CYS.  
 FT REPEAT 31 65 TNFR-CYS 1.  
 FT REPEAT 66 107 TNFR-CYS 2.  
 FT REPEAT 108 147 TNFR-CYS 3.  
 FT REPEAT 148 189 TNFR-CYS 4.  
 FT DOMAIN 344 421 DEATH DOMAIN.  
 FT DISULFID 32 43 BY SIMILARITY.  
 FT DISULFID 44 57 BY SIMILARITY.  
 FT DISULFID 47 64 BY SIMILARITY.  
 FT DISULFID 67 83 BY SIMILARITY.  
 FT DISULFID 86 99 BY SIMILARITY.  
 FT DISULFID 89 107 BY SIMILARITY.  
 FT DISULFID 109 122 BY SIMILARITY.  
 FT DISULFID 125 138 BY SIMILARITY.  
 FT DISULFID 128 146 BY SIMILARITY.  
 FT DISULFID 149 164 BY SIMILARITY.  
 FT DISULFID 167 180 BY SIMILARITY.  
 FT DISULFID 170 188 BY SIMILARITY.  
 FT DOMAIN 197 248 SER/THR-RICH.  
 FT CARBOHYD 60 60 POTENTIAL.  
 SQ SEQUENCE 427 AA; 45183 MW; EE2924BD CRC32;

Query Match 6.8%; Score 185; DB 1; Length 427;  
 Best Local Similarity 29.4%; Pred. No. 4.71e-15;  
 Matches 25; Conservative 21; Mismatches 37; Indels 2; Gaps 2;

Db 64 CEPCLDSVTFSDDVVSAPECPCKCTECVGLQSMSAPCVAADDAVCRCAYGYQD-ETTGRC 122  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTRDTVCQCEKGSFQDKNSPEMC 155

Db 123 EACRV-CEAGSGLVFSQDKQNTVC 146  
 ||| :| | | :| :| :|  
 Qy 156 RTCRTGCPGRGMVKVSNCNTPRSDIKC 180

RESULT 6  
 ID TNRL\_PIG STANDARD; PRT; 461 AA:  
 AC P50555;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).  
 GN TNFR1.  
 OS SUS SCROFA (PIG).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; ARTIODACTyla.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-KIDNEY;  
 RX MEDLINE; 96011645.  
 RA SUTER B., PAULI U.H.;  
 RL GENE 163:263-266(1995).  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; U19994; G1141753; -.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR 1.  
 FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 211 233 POTENTIAL.  
 FT DOMAIN 234 461 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 43 195 4 X TNFR-CYS.  
 FT REPEAT 43 82 TNFR-CYS 1.  
 FT REPEAT 83 125 TNFR-CYS 2.  
 FT REPEAT 126 166 TNFR-CYS 3.  
 FT REPEAT 167 195 TNFR-CYS 4.  
 FT DOMAIN 362 447 DEATH DOMAIN.  
 FT DISULFID 44 58 BY SIMILARITY.  
 FT DISULFID 59 72 BY SIMILARITY.  
 FT DISULFID 62 81 BY SIMILARITY.  
 FT DISULFID 84 99 BY SIMILARITY.  
 FT DISULFID 102 117 BY SIMILARITY.  
 FT DISULFID 105 125 BY SIMILARITY.  
 FT DISULFID 127 143 BY SIMILARITY.  
 FT DISULFID 146 158 BY SIMILARITY.  
 FT DISULFID 149 166 BY SIMILARITY.  
 FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 190 BY SIMILARITY.  
 FT DISULFID 185 194 BY SIMILARITY.  
 FT CARBOHYD 54 54 POTENTIAL.  
 FT CARBOHYD 86 86 POTENTIAL.  
 FT CARBOHYD 145 145 POTENTIAL.  
 FT CARBOHYD 151 151 POTENTIAL.  
 SO SEQUENCE 461 AA: 50696 MW: 88293504 CRC32:

Query Match 6.8%; Score 184; DB 1; Length 461;  
Best Local Similarity 36.3%; Pred. No. 7.22e-15;  
Matches 33; Conservative 17; Mismatches 32; Indels 9; Gaps 7;

Db 81 CRECDNGT-FTASENHLTQCLSCSKCRSEMSQVEISPCTVDRDTVCGRKNQYR-KYWSE 138

Qy 96 CNPCTEGVDYTIASNNLPSCLLCTVCKS--GQTNKSSCTTRDTCQCCEKGSFQDKNSPE 153  
 Db 139 TLFQCLNCSL-CPNGTVQLP-CLEKQDTICN 167  
     : | | ||| :: | : | : |:  
 Qy 154 -M--CRTCRTGCPRGMVKSNCPRSDIKCK 181

**RESULT** 7

ID VT2\_MYXVL STANDARD; PRT; 326 AA.  
 AC P29825;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).  
 GN T2.  
 OS MYXOMA VIRUS (STRAIN LAUSANNE).  
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPHOXVIRINAE;  
 OC LEPORIPOROVIRUSES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91335768.  
 RA UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;  
 RL VIROLOGY 184:370-382(1991).  
 CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO  
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL  
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; M95181; G332310; -.  
 DR EMBL; A23729; E199442; -.  
 DR PIR; AA0566; GQVZML.  
 DR HSSP; P19438; 1TNR.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 326 PROTEIN T2.  
 FT DOMAIN 27 186 4 X TNFR-CYS.  
 FT REPEAT 27 62 TNFR-CYS 1.  
 FT REPEAT 63 104 TNFR-CYS 2.  
 FT REPEAT 105 147 TNFR-CYS 3.  
 FT REPEAT 148 186 TNFR-CYS 4.  
 FT CARBOHYD 66 66 POTENTIAL.  
 FT CARBOHYD 181 181 POTENTIAL.  
 FT CARBOHYD 205 205 POTENTIAL.  
 FT CARBOHYD 238 238 POTENTIAL.  
 SQ SEQUENCE 326 AA; 35208 MW; 2F059A61 CRC32;

Query Match 6.6%; Score 180; DB 1; Length 326;  
 Best Local Similarity 34.4%; Pred. No. 3.95e-14;  
 Matches 31; Conservative 20; Mismatches 34; Indels 5; Gaps 4;

61 CSPCKNET-FTASTNHAPACVSCRGRTGHLSESQSCKTRDVCDCSAGNYCLLKGQEG 119  
|::| : |::| :||: |::| : |::| : |||::| |||::| :||: ::|  
96 CNPCTEGVDYTIASSNLPLSCLLCTV-CKSQTNKSSCTTTRDTCQCCEKGSFQDKNSPEM 154

0b 120 CRICAPTKCPAGYG-VSGHTRTGDVLCTK 148

155 GPTG RTGGCGGCGAGKVKVSNCTTBBGSDIKCKN 182

RESULT 8  
ID FASA\_MOUSE STANDARD; PRT; 327 AA.  
AC P25446;  
DT 01-MAY-1992 (REL. 22, CREATED)  
DT 01-MAY-1992 (REL 22, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL 35, LAST ANNOTATION UPDATE)  
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)  
DE (APO-1 ANTIGEN) (CD95).  
GN APT1 OR FAS.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92148151.  
 RA WATANABE-FUKUNAGA R., BRANNAN C.I., ITOH N., YONEHARA S.,  
 RA COPELAND N.G., JENKINS N.A., NAGATA S.;  
 RL J. IMMUNOL. 148:1274-1279(1992).  
 RN [2]  
 RP SEQUENCE OF 1-96 FROM N.A.  
 RX MEDLINE; 93189576.  
 RA ADACHI M., WATANABE-FUKUNAGA R., NAGATA S.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:1756-1760(1993).  
 RN [3]  
 RP VARIANT LPR.  
 RX MEDLINE; 92195401.  
 RA WATANABE-FUKUNAGA R., BRANNAN C.I., COPELAND N.G., JENKINS N.A.,  
 RA NAGATA S.;  
 RL NATURE 356:314-317(1992).  
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE  
 CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED  
 CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH- INDUCING  
 CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC  
 CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF  
 CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING  
 CC APOPTOSIS. FAS- MEDiated APOPTOSIS MAY HAVE A ROLE IN THE  
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED  
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,  
 CC LIVER, LUNG, HEART, AND ADULT OVARY.  
 CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC -!- DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION  
 CC DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY  
 CC PRODUCTION.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; M83649; G193226; -.  
 DR EMBL; S56490; G298506; -.  
 DR EMBL; S56485; G298506; JOINED.  
 DR EMBL; S56486; G298506; JOINED.  
 DR PIR; A46484; A46484.  
 DR HSSP; P19438; 1TNR.  
 DR MGD; MGI:95484; FAS.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL;  
 KW DISEASE MUTATION.  
 FT SIGNAL 1 21  
 FT CHAIN 22 327 FASL RECEPTOR.  
 FT DOMAIN 22 169 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 170 186 POTENTIAL.  
 FT DOMAIN 187 327 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 43 162 3 X TNFR-CYS.  
 FT REPEAT 43 79 TNFR-CYS 1.  
 FT REPEAT 80 123 TNFR-CYS 2.  
 FT REPEAT 124 162 TNFR-CYS 3.  
 FT DOMAIN 222 306 DEATH DOMAIN.  
 FT CARBOHYD 43 43 POTENTIAL.  
 FT CARBOHYD 114 114 POTENTIAL.  
 FT VARIANT 246 246 I -> N (IN LPR).  
 SQ SEQUENCE 327 AA; 37418 MW; 22D6DC39 CRC32;

Query Match 6.5%; Score 177; DB 1; Length 327;  
 Best Local Similarity 30.5%; Pred. No. 1.40e-13;  
 Matches 29; Conservative 25; Mismatches 36; Indels 5; Gaps 5;  
 Db 75 TPTCAPCTEGKEYMDKNHYADKCRCTLCDDEHGLEVETNCLTQNTKCKCKPDFYCDSP 134  
 | : | |||| : | :: | ||:| : : ::|| |::| | | : |  
 Qy 93 TGACNPCTEGVDYTIASNNLPSCLLCTVKSGQT-N-KSSCTTTRDTVCQCEKGFSQDKN 150  
 Db 135 GCEHCVRCA-ASCEHGTL-P-CTATSNTNCRKQSP 166  
 : | | | ::| : : ||: | : ::||:  
 Qy 151 SPEMCRTCRTGCPGRMVKVSNCTPRSDIKCKNESA 185

RESULT 9  
 ID TNFR1\_HUMAN STANDARD PRT; 455 AA.  
 AC P19438;  
 DT 01-FEB-1991 (REL. 17, CREATED)  
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR  
 DE BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (P55) (CD120A).  
 GN TNFR1 OR TNFR.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RX MEDLINE; 90235285.  
 RA SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,  
 RA GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;  
 RL CELL 61:361-370(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 90235284.  
 RA LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,  
 RA TABUCHI H., LESSLAUER W.;  
 RL CELL 61:351-359(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.  
 RX MEDLINE; 9106021.  
 RA NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,  
 RA ADERKA D., HOLTMANN H., WALLACH D.;  
 RL EMBO J. 9:3269-3278(1990).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91090841.  
 RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,  
 RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;  
 RL DNA CELL BIOL. 9:705-715(1990).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RX MEDLINE; 91017509.  
 RA GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92250049.  
 RA FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;  
 RL GENOMICS 13:219-224(1992).  
 RN [7]  
 RP SEQUENCE OF 41-45.  
 RX MEDLINE; 90110215.  
 RA ENGELMANN H., NOVICK D., WALLACH D.;  
 RL J. BIOL. CHEM. 265:1531-1536(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.  
 RX MEDLINE; 93258809.  
 RA BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,  
 RA BROGER C., LOETSCHER H., LESSLAUER W.;  
 RL CELL 73:431-445(1993).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 RX MEDLINE; 97094982.  
 RA NAISMITH J.H., DEVINE T.O., KHONO H., SPRANG S.R.;  
 RL STRUCTURE 4:1251-1262(1996).  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS.  
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

DR EMBL; X55313; G37224; -.  
 DR EMBL; M33294; G339745; -.  
 DR EMBL; M58286; G339754; -.  
 DR EMBL; M63121; G339756; -.  
 DR EMBL; M75866; G339750; -.  
 DR EMBL; M75864; G339750; JOINED.

DR EMBL; M75865; G339750; JOINED.  
 DR EMBL; M60275; G339760; -.  
 DR EMBL; A21522; G579600; -.  
 DR PIR; A34899; GQHUT1.  
 DR PIR; A35010; A35010.  
 DR PIR; S12057; S12057.  
 DR PIR; A38208; A38208.  
 DR PDB; 1TNR; 31-JUL-94.  
 DR PDB; 1NCF; 07-DEC-95.  
 DR PDB; 1EXT; 11-JAN-97.  
 DR MIM; 191190; -.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.

KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;  
 KW 3D-STRUCTURE.

FT SIGNAL 1 21  
 FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR 1.  
 FT DOMAIN 41 291 TUMOR NECROSIS FACTOR BINDING PROTEIN 1.  
 FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 212 234 POTENTIAL.  
 FT DOMAIN 235 455 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 43 196 4 X TNFR-CYS.  
 FT REPEAT 43 82 TNFR-CYS 1.  
 FT REPEAT 83 125 TNFR-CYS 2.  
 FT REPEAT 126 166 TNFR-CYS 3.  
 FT REPEAT 167 196 TNFR-CYS 4.  
 FT DOMAIN 356 441 DEATH DOMAIN.  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 191  
 FT DISULFID 185 195  
 FT CARBOHYD 54 54 POTENTIAL.  
 FT CARBOHYD 145 145 POTENTIAL.  
 FT CARBOHYD 151 151 POTENTIAL.  
 FT CONFLICT 412 412 MISSING (IN REF. 4).  
 FT CONFLICT 443 446 GPAA -> APP (IN REF. 4).  
 SQ SEQUENCE 455 AA; 50494 MW; CE0EA06F CRC32;

Query Match 6.4%; Score 173; DB 1; Length 455;  
 Best Local Similarity 37.1%; Pred. No. 7.47e-13;  
 Matches 33; Conservative 12; Mismatches 37; Indels 7; Gaps 6;

Db 81 CRECESG-SFTASENHLRHCLCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHYSEN 139  
 | | | : | : | || : | : | || | : | : | | : | :

Qy 96 CNPCTEGVDYTIASNNLPSCLLCTVC-KS-GQTNKSSCTTRDTVCQCEKGSPQDKNSPE 153

Db 140 LFQCFNCSL-CLNGLTVHLS-CQEKNQNTVC 166

: | | | | : | : | : | :

Qy 154 M--CRTCRTGCPGRGMVKVSNCPRSDIKC 180

RESULT 10  
 ID NGFR\_CHICK STANDARD; PRT; 416 AA.  
 AC P18519;  
 DT 01-NOV-1990 (REL. 16, CREATED)  
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
 DE (GP80-LNGFR).  
 GN NGFR.  
 OS GALLUS GALLUS (CHICKEN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;  
 OC GALLIFORMES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE; 90166579.  
 RA LARGE T.H., WESKAMP G., HELDER J.C., RADEKE M.J., MISKO T.P.,  
 RA SHOOTER E.M., REICHARDT L.F.;  
 RL NEURON 2:1123-1134(1989).  
 RN [2]  
 RP SEQUENCE OF 21-416 FROM N.A.  
 RX MEDLINE; 90152140.  
 RA HEUER J.G., FATEMIE-NAINIE S., WHEELER E.F., BOTHWELL M.;  
 RL DEV. BIOL. 137:287-304(1990).  
 CC -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 CC NT-3, AND NT-4.  
 CC -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE  
 CC BOND FORMATION.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR PIR; JN0006; JN0006.  
 DR PIR; A60504; A60504.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;  
 KW PHOSPHORYLATION; SIGNAL.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 416 NGF RECEPTOR.  
 FT DOMAIN 29 239 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 240 261 POTENTIAL.  
 FT DOMAIN 262 416 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 23 181 4 X TNFR-CYS.  
 FT REPEAT 23 57 TNFR-CYS 1.  
 FT REPEAT 58 100 TNFR-CYS 2.  
 FT REPEAT 101 140 TNFR-CYS 3.  
 FT REPEAT 141 181 TNFR-CYS 4.  
 FT DOMAIN 188 236 SER/THR-RICH.  
 FT DOMAIN 333 410 DEATH DOMAIN.  
 FT DISULFID 24 35 BY SIMILARITY.  
 FT DISULFID 36 49 BY SIMILARITY.  
 FT DISULFID 39 56 BY SIMILARITY.  
 FT DISULFID 59 75 BY SIMILARITY.  
 FT DISULFID 78 91 BY SIMILARITY.  
 FT DISULFID 81 99 BY SIMILARITY.  
 FT DISULFID 101 114 BY SIMILARITY.  
 FT DISULFID 117 130 BY SIMILARITY.  
 FT DISULFID 120 138 BY SIMILARITY.  
 FT DISULFID 141 156 BY SIMILARITY.  
 FT DISULFID 159 172 BY SIMILARITY.  
 FT DISULFID 162 180 BY SIMILARITY.  
 FT CARBOHYD 52 52 POTENTIAL.  
 FT CONFLICT 36 36 C -> Y (IN REF. 2).  
 FT CONFLICT 173 173 T -> K (IN REF. 2).  
 FT CONFLICT 276 276 N -> S (IN REF. 2).  
 FT CONFLICT 396 396 K -> R (IN REF. 2).  
 SQ SEQUENCE 416 AA; 44654 MW; 4D3F086A CRC32;

Query Match 6.3%; Score 170; DB 1; Length 416;  
 Best Local Similarity 30.6%; Pred. No. 2.60e-12;  
 Matches 26; Conservative 17; Mismatches 40; Indels 2; Gaps 2;

Db	56	CEPCLSDSVTYSDTVSATEPCKPCTQCVGLHSMAPCVESDDAVCRCAYGQFQDELSGS-C	114
	:	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Qy	96	CNPCTEGVDYTIASSLNLPSCLLCTVCKSGQTNKSSCTTRDVTVCQCEKGFSQDKNSPEMC	155
Db	115	KECSI-CEVGFGLMFPPCRDSQDTVC	138
	:	:   :   :   :	.
Qy	156	RTCRTGCPGRGMVKVSNTPRSDIKC	180

RESULT 11  
ID NGFR\_RAT STANDARD; PRT; 425 AA.  
AC P07174;  
DT 01-APR-1988 (REL. 07, CREATED)  
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
DE (GP80-LNGFR).  
GN NGFR.  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 87115859.  
RA RADEKE M.J., MISKO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M.;  
RL NATURE 325:593-597(1987).  
RN [2]  
RP SEQUENCE OF 1-22 FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE; 93077038.  
RA METSIS M., TIMMUSK T., ALLIKMETS R., SAARMA M., PERSSON H.;  
RL GENE 121:247-254(1992).  
RN [3]  
RP STRUCTURE BY NMR OF 334-418.  
RA LIEPINSH E., ILAG L., OTTING G., IBANEZ C.;  
RL SUBMITTED (JAN-1997) TO THE PDB DATA BANK.  
CC -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
CC NT-3, AND NT-4.  
CC -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE  
CC BOND FORMATION.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL; X05137; G56756; -.  
DR EMBL; X61269; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A26431; A26431.  
DR PDB; 1NGR; 29-JUL-97.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;  
KW PHOSPHORYLATION; SIGNAL; 3D-STRUCTURE.

FT	SIGNAL	1	29	
FT	CHAIN	30	425	NGF RECEPTOR.
FT	DOMAIN	30	251	EXTRACELLULAR
FT	TRANSMEM	252	273	POTENTIAL.
FT	DOMAIN	274	425	CYTOPLASMIC (P
FT	DOMAIN	32	190	4 X TNFR-CYS.
FT	REPEAT	32	66	TNFR-CYS 1.
FT	REPEAT	67	108	TNFR-CYS 2.
FT	REPEAT	109	148	TNFR-CYS 3.
FT	REPEAT	149	190	TNFR-CYS 4.
FT	DOMAIN	198	249	SER/THR-RICH.
FT	DOMAIN	354	419	DEATH DOMAIN.
FT	DISULFID	33	44	BY SIMILARITY.
FT	DISULFID	45	58	BY SIMILARITY.
FT	DISULFID	48	65	BY SIMILARITY.
FT	DISULFID	68	84	BY SIMILARITY.
FT	DISULFID	87	100	BY SIMILARITY.
FT	DISULFID	90	108	BY SIMILARITY.
FT	DISULFID	110	123	BY SIMILARITY.
FT	DISULFID	126	139	BY SIMILARITY.

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FT  DISULFID  129  147      BY SIMILARITY.
FT  DISULFID  150  165      BY SIMILARITY.
FT  DISULFID  168  181      BY SIMILARITY.
FT  DISULFID  171  189      BY SIMILARITY.
FT  CARBOHYD   61   61      POTENTIAL.
FT  CARBOHYD   71   71      POTENTIAL.
SQ  SEQUENCE 425 AA; 45432 MW; 7D78F258 CRC32;

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Query Match 6.3%; Score 171; DB 1; Length 425;  
Best Local Similarity 28.2%; Pred. No. 1 72e-12;

RESULT 12  
ID VT2\_SFVKA STANDARD; PRT; 325 AA.  
AC P25943;  
DT 01-MAY-1992 (REL. 22, CREATED)  
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)  
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)  
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).  
GN T2.  
OS SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).  
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINA  
OC LEPORIPORIVIRUSES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 87321103.  
RA UPTON C., DELANGE A.M., MCFADDEN G.;  
RL VIROLOGY 160:20-30(1987).  
RN [2]  
RP FUNCTION.  
RX MEDLINE; 91207415.  
RA SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARAH T., UPTON  
RA MCFADDEN G., GOODWIN R.G.;  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).  
CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS THE  
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL  
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.  
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REG  
CC TURE (115/120). NOT ALIGNMENT OF

DR EMBL; M17433; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; A23727; E199408; -.  
 DR PIR; B43692; B43692.  
 DR HSPP; P19438; 1TNR.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 325 PROTEIN T2.  
 FT DOMAIN 27 186 4 X TNFR-CYS.  
 FT REPEAT 27 62 TNFR-CYS 1.  
 FT REPEAT 63 104 TNFR-CYS 2.  
 FT REPEAT 105 147 TNFR-CYS 3.  
 FT REPEAT 148 186 TNFR-CYS 4.  
 FT CARBOHYD 105 105 POTENTIAL.  
 FT CARBOHYD 181 181 POTENTIAL.  
 FT CARBOHYD 205 205 POTENTIAL.  
 FT CARBOHYD 238 238 POTENTIAL.  
 SO SEQUENCE 325 AA; 35132 MW: C9d2C87B CRC32;

QY 96 CNPCTEGVDYTIASNLPSCLLC-TVCKSGQTNKSSCTTTRDTVCQCEKGSFQDKNSPEM 154  
 Db 120 CRICAPQTCKCPAGVG-VSGHTRAGDTLC 146  
 ||| :||| || | :|||  
 Qy 155 CRTC--RTGCPRGMVKVSNCPRSDIIC 180

**RESULT 13**  
 ID TNFR1\_RAT STANDARD; PRT; 461 AA.  
 AC P22934;  
 DT 01-AUG-1991 (REL. 19, CREATED)  
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).  
 GN TNFR1 OR TNFR-1.  
 OS RATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91090841.  
 RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,  
 RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;  
 RL DNA CELL BIOL. 9:705-715(1990).  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; M63122; G207362; -.  
 DR PIR; B36555; B36555.  
 DR HSSP; P19438; 1TNR.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR 1.  
 FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 212 234 POTENTIAL.  
 FT DOMAIN 235 461 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 43 196 4 X TNFR-CYS.  
 FT REPEAT 43 82 TNFR-CYS 1.  
 FT REPEAT 83 125 TNFR-CYS 2.  
 FT REPEAT 126 166 TNFR-CYS 3.  
 FT REPEAT 167 196 TNFR-CYS 4.  
 FT DOMAIN 363 448 DEATH DOMAIN.  
 FT DISULFID 44 58 BY SIMILARITY.  
 FT DISULFID 59 72 BY SIMILARITY.  
 FT DISULFID 62 81 BY SIMILARITY.  
 FT DISULFID 84 99 BY SIMILARITY.  
 FT DISULFID 102 117 BY SIMILARITY.  
 FT DISULFID 105 125 BY SIMILARITY.  
 FT DISULFID 127 143 BY SIMILARITY.  
 FT DISULFID 146 158 BY SIMILARITY.  
 FT DISULFID 149 166 BY SIMILARITY.  
 FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 191 BY SIMILARITY.  
 FT DISULFID 185 195 BY SIMILARITY.  
 FT CARBOHYD 54 54 POTENTIAL.  
 FT CARBOHYD 151 151 POTENTIAL.  
 FT CARBOHYD 201 201 POTENTIAL.

CC LEVEL ON THREONINE RESIDUES.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; M32315; G189186; -.  
 DR EMBL; M35857; G339752; -.  
 DR EMBL; U52165; G1469541; -.  
 DR EMBL; U52156; G1469541; JOINED.  
 DR EMBL; U52157; G1469541; JOINED.  
 DR EMBL; U52158; G1469541; JOINED.  
 DR EMBL; U52159; G1469541; JOINED.  
 DR EMBL; U52160; G1469541; JOINED.  
 DR EMBL; U52161; G1469541; JOINED.  
 DR EMBL; U52162; G1469541; JOINED.  
 DR EMBL; U52163; G1469541; JOINED.  
 DR EMBL; U52164; G1469541; JOINED.  
 DR EMBL; M55994; G339758; -.  
 DR PIR; A35356; A35356.  
 DR PIR; A36007; A36007.  
 DR PIR; A36475; A36475.  
 DR PIR; B35010; B35010.  
 DR PIR; A23666; A23666.  
 DR HSSP; P19438; 1TNR.  
 DR MIM; 191191; -.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;  
 KW PHOSPHORYLATION.  
 FT SIGNAL 1 22  
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 258 287 POTENTIAL.  
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 201 4 X TNFR-CYS.  
 FT REPEAT 39 76 TNFR-CYS 1.  
 FT REPEAT 77 118 TNFR-CYS 2.  
 FT REPEAT 119 162 TNFR-CYS 3.  
 FT REPEAT 163 201 TNFR-CYS 4.  
 FT DISULFID 40 53 BY SIMILARITY.  
 FT DISULFID 54 67 BY SIMILARITY.  
 FT DISULFID 57 75 BY SIMILARITY.  
 FT DISULFID 78 93 BY SIMILARITY.  
 FT DISULFID 96 110 BY SIMILARITY.  
 FT DISULFID 100 118 BY SIMILARITY.  
 FT DISULFID 120 126 BY SIMILARITY.  
 FT DISULFID 134 143 BY SIMILARITY.  
 FT DISULFID 137 161 BY SIMILARITY.  
 FT DISULFID 164 179 BY SIMILARITY.  
 FT CARBOHYD 171 171 POTENTIAL.  
 FT CARBOHYD 193 193 POTENTIAL.  
 FT CONFLICT 141 141 R -> P (IN REF. 4).  
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).  
 FT CONFLICT 363 363 A -> T (IN REF. 4).  
 SQ SEQUENCE 461 AA; 48316 MW; 0F5D0C44 CRC32;

Query Match 5.8%; Score 158; DB 1; Length 461;  
 Best Local Similarity 27.9%; Pred. No. 3.51e-10;  
 Matches 29; Conservative 23; Mismatches 48; Indels 4; Gaps 3;

Db 75 CDSCEDST-YTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTRCPGWYCALSKQEG 133  
 ||::| :: || | :||| : ||| : :|| ::|| | : : |  
 Qy 96 CNPCTEGVDYTIASNNLPSCLLC-TVCKSGQTNKSSCTTRDTCQCCEKGFSQDKNSPEM 154  
 Db 134 CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNNTSSTD 177  
 ||| | | | | | : || ::| : |::: |:::  
 Qy 155 CRTCRT--GCPRGMVKVNCTPRSDIKCKNESASAATGKTPAAE 196

RESULT 15  
 ID TNFR\_MOUSE STANDARD; PRT; 454 AA.  
 AC P25118;  
 DT 01-MAY-1992 (REL. 22, CREATED)  
 DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).

GN TNFR1 OR TNFR-1.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91187885.  
 RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,  
 RA WONG G.H., CHEN E.Y., GOEDDEL D.V.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91246168.  
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,  
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.;  
 RL MOL. CELL. BIOL. 11:3020-3026(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91285014.  
 RA BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,  
 RA GRAY P.W., FELDMANN M., FOXWELL B.M.J.;  
 RL EUR. J. IMMUNOL. 21:1649-1656(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RX MEDLINE; 92039815.  
 RA ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;  
 RL IMMUNOGENETICS 34:338-340(1991).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 94245292.  
 RA BEBO B.F., LINTHICUM D.S.;  
 RL IMMUNOGENETICS 39:450-451(1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 93156721.  
 RA ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;  
 RL MOL. IMMUNOL. 30:165-175(1993).  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; M60468; G199826; -.  
 DR EMBL; M59377; G202097; -.  
 DR EMBL; X59238; G53579; -.  
 DR EMBL; X57796; G54849; -.  
 DR EMBL; L26349; G430733; -.  
 DR EMBL; M76656; G202102; -.  
 DR EMBL; M88067; G202102; JOINED.  
 DR EMBL; M76655; G202102; JOINED.  
 DR PIR; A38634; GQMST1.  
 DR PIR; S16677; S16677.  
 DR PIR; S19021; S19021.  
 DR HSSP; P19438; 1TNR.  
 DR MGD; MGI:98781; TNFR1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.

FT DOMAIN	22	212	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	213	235	POTENTIAL.
FT DOMAIN	236	454	CYTOPLASMIC (POTENTIAL).
FT DOMAIN	43	196	4 X TNFR-CYS.
FT REPEAT	43	82	TNFR-CYS 1.
FT REPEAT	83	125	TNFR-CYS 2.
FT REPEAT	126	166	TNFR-CYS 3.
FT REPEAT	167	196	TNFR-CYS 4.
FT DOMAIN	356	441	DEATH DOMAIN.
FT DISULFID	44	58	BY SIMILARITY.
FT DISULFID	59	72	BY SIMILARITY.
FT DISULFID	62	81	BY SIMILARITY.
FT DISULFID	84	99	BY SIMILARITY.
FT DISULFID	102	117	BY SIMILARITY.
FT DISULFID	105	125	BY SIMILARITY.
FT DISULFID	127	143	BY SIMILARITY.
FT DISULFID	146	158	BY SIMILARITY.
FT DISULFID	149	166	BY SIMILARITY.
FT DISULFID	168	179	BY SIMILARITY.
FT DISULFID	182	191	BY SIMILARITY.
FT DISULFID	185	195	BY SIMILARITY.
FT CARBOHYD	54	54	POTENTIAL.
FT CARBOHYD	151	151	POTENTIAL.
FT CARBOHYD	202	202	POTENTIAL.
FT CONFLICT	394	394	R -> G (IN REF. 6).
SQ SEQUENCE	454 AA;	50129 MW;	4B6EEC09 CRC32;

Query Match 5.7%; Score 156; DB 1; Length 454;  
 Best Local Similarity 30.8%; Pred. No. 7.85e-10;  
 Matches 32; Conservative 17; Mismatches 44; Indels 11; Gaps 11;

Db	71 DCPSPG-R-D-T-VCRECEKGT-FTASQNYLRQCLSCKTCRKEMSQVEISPCQADKDTVC 125 : : :  :        :  :           :  :  :  :
Qy	82 ECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCVCKS-GQTNKSSCTTRDTVC 139
Db	126 GCKENQFORYLSETHFQCVDC-SPCFNGTVTIP-CKETQNTVCN 167       :     :         ;   :
Qy	140 QCEKGGSFQDKNSPEM-CRTCRTGCPRGMVKVSNCTPRSDIKCK 181

Search completed: Thu May 14 16:47:55 1998  
 Job time : 22 secs.

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MPsrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri May 15 18:56:00 1998; MasPar time 262.16 Seconds  
916.449 Million cell updates/sec

Tabular output not generated.

Title: >US-08-918-874-2

Description: (1-2082) from US08918874.seq

Perfect Score: 2082

N.A. Sequence: 1 CCAACTGACCTCGTTCTA.....CATTTATATTGCTTACTA 2082  
 Comp: GGTGACGTGGAGCCAAGAT.....GTAAAAATAACGAAATGAT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-geneseq30

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.752; Variance 5.463; scale 1.785

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query						Description	Pred. No.
	No.	Score	Match	Length	DB	ID		
c	1	85	4.1	335	8	Q61099	Human brain Expressed	4.21e-39
c	2	85	4.1	22481	24	T11658	PEDF full length sequ	4.21e-39
	3	83	4.0	2477	24	T38689	Human CRTAM.	1.01e-37
c	4	83	4.0	2562	28	T59650	Human dsRNA-dependent	1.01e-37
c	5	83	4.0	2562	15	T03903	Human p68 kinase mRNA	1.01e-37
c	6	84	4.0	3234	15	Q92781	Human thymopoietin ge	2.07e-38
	7	81	3.9	1047	2	Q10572	Human Natriuretic Pep	2.42e-36
c	8	82	3.9	1047	2	Q10572	Human Natriuretic Pep	4.96e-37
	9	81	3.9	1618	7	Q46958	Human cytokine synthet	2.42e-36
	10	81	3.9	1618	2	Q10207	pH15C insert containi	2.42e-36
	11	82	3.9	17327	7	Q44278	Serglycin - proteoglyc	4.96e-37
	12	80	3.8	429	8	Q60835	Human brain Expressed	1.18e-35
	13	79	3.8	1830	17	T03731	TNF-R p75IC-binding p	5.73e-35
	14	79	3.8	8342	13	Q75209	ALL-1 (acute lymphocy	5.73e-35
	15	79	3.8	8391	19	T16333	MLL gene 8.3 kb fragm	5.73e-35

16	79	3.8	8392	9	Q53478	MLL gene 8.3 kb BamHI	5.73e-35	
17	79	3.8	24025	21	T17515	Mutated BRCA1 genomic	5.73e-35	
18	79	3.8	24025	21	T17455	Mutated BRCA1 genomic	5.73e-35	
19	79	3.8	24026	21	T17527	Mutated BRCA1 genomic	5.73e-35	
20	79	3.8	24026	21	T17517	Mutated BRCA1 genomic	5.73e-35	
21	79	3.8	24026	21	T17526	Mutated BRCA1 genomic	5.73e-35	
22	79	3.8	24026	21	T17522	Mutated BRCA1 genomic	5.73e-35	
23	79	3.8	24026	21	T17516	Mutated BRCA1 genomic	5.73e-35	
24	79	3.8	24026	21	T17523	Mutated BRCA1 genomic	5.73e-35	
25	79	3.8	24026	21	T17514	Mutated BRCA1 genomic	5.73e-35	
26	79	3.8	24026	21	T17521	Mutated BRCA1 genomic	5.73e-35	
27	79	3.8	24026	21	T17524	Mutated BRCA1 genomic	5.73e-35	
28	79	3.8	24026	21	T17528	Mutated BRCA1 genomic	5.73e-35	
29	79	3.8	24026	21	T17530	BRCA1 genomic sequenc	5.73e-35	
30	79	3.8	24026	21	T17513	Mutated BRCA1 genomic	5.73e-35	
31	79	3.8	24026	23	T32612	BRCA1, human breast a	5.73e-35	
32	79	3.8	24026	21	T17519	Mutated BRCA1 genomic	5.73e-35	
33	79	3.8	24026	18	T18325	BRCA1, human breast a	5.73e-35	
34	79	3.8	24026	21	T17529	Mutated BRCA1 genomic	5.73e-35	
35	79	3.8	24026	21	T17518	Mutated BRCA1 genomic	5.73e-35	
36	79	3.8	24026	21	T17512	Mutated BRCA1 genomic	5.73e-35	
37	79	3.8	24029	21	T17520	Mutated BRCA1 genomic	5.73e-35	
38	79	3.8	24031	21	T17525	Mutated BRCA1 genomic	5.73e-35	
c	39	80	3.8	30967	23	T32454	Calpain large subunit	1.18e-35
40	78	3.7	1926	33	T73340	Human GADII cDNA.	2.77e-34	
41	77	3.7	6210	11	Q63815	c-fos gene.	1.34e-33	
42	78	3.7	11298	33	T87656	Human high affinity I	2.77e-34	
43	78	3.7	11357	9	Q51024	Human Fc <sub>ERI</sub> beta chai	2.77e-34	
44	78	3.7	30967	23	T32454	Calpain large subunit	2.77e-34	
c	45	78	3.7	53577	28	T18551	Human polycystic kidn	2.77e-34

## ALIGNMENTS

**RESULT** 1  
ID Q61099 standard; DNA; 335 BP.  
AC Q61099;  
DT 16-MAR-1994 (first entry)  
DE Human brain Expressed Sequence Tag EST01693.  
KW Gene transcription product; genetic markers; tagging; in vivo;  
KW transcription; mapping; locations; chromosomes; chromosomal; ss.  
OS Homo sapiens.  
PN WO9316178-A.  
PD 19-AUG-1993.  
PF 12-FEB-1993; U01294.  
PR 12-FEB-1992; US-837195.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
PI Adams MD, Moreno RF, Venter CJ.  
DR WPI; 93-272882/34.  
PT Enriched oligonucleotides and corresp. sequences - used as  
PT markers for human genes transcribed in-vivo, facilitate tagging  
PT of most human genes  
PS Example 4; Page 438; 500pp; English.  
CC The Expressed Sequence Tag was isolated from a human brain cDNA  
CC library as part of a large set of ESTs which can be used as markers  
CC for human genes transcribed in vivo. They can be used to facilitate  
CC tagging of most human genes, for mapping locations of expressed genes  
CC on chromosomes, for individual or forensic identification, for mapping  
CC locations of disease-associated genes, for identification of tissue  
CC type, and for prepn. of antisense sequences, probes and constructs.  
CC EST01693 has a "Poor" coding probability as evaluated using the  
CC coding-region prediction program CRM. See also Q59041-Q61440.  
SQ Sequence 335 BP; 77 A; 94 C; 82 G; 79 T;  
  
Query Match 4.1%; Score 85; DB 8; Length 335;  
Best Local Similarity 80.7%; Pred. No. 4.21e-39;  
Matches 109; Conservative 0; Mismatches 26; Indels 0; Gaps 0  
  
Db 151 tttttntnatttttgtagagacgggttccacctgtggccaggctggctcaaaactc 210  
||| ||||| ||||| ||||| ||||| ||||| |||||  
Cp 1716 TTTTTTCTTTAAATTGAGATGGAGTTCACTGTGTTGATGAGGCTGGCTCAAACTC 1657  
  
Db 211 ctgaaqctcaagcaatctggccacctaagccctcaaaaqtgtcqgcattacaggcatqagc 270

Cp	1656	CCGAGCTCAAGCAATCCACCTGCCTCAGCCTATCAAAGTGCCTGGGATTACAGGCATGAGC	1597
Db	271	caccgtgcctggcct	285
Cp	1596	CACCGCATGTGGCCT	1582

RESULT 2  
ID T11658 standard; DNA; 22481 BP.  
AC T11658;  
DT 16-JAN-1997 (first entry)  
DE PEDF full length sequence and flanking sequences.  
KW Pigment epithelium-derived factor; PEDF; neuronal cells; neurons;  
KW glial cells; gliostatic; gliosis; central nervous system; CNS;  
KW neurodegenerative disease; injury; neuronotrophic; brain cells;  
KW Parkinson's disease; photoreceptor cells; retina; inhibition;  
KW proliferation; immunoassay; antibody; ageing; degenerative disease;  
KW ds.  
OS Homo sapiens.  
PN WO9533480-A1.  
PD 14-DEC-1995.  
PF 06-JUN-1995; U07201.  
PR 07-JUN-1994; US-257963.  
PR 30-DEC-1994; US-367841.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PI Becerra SP, Chader GJ, Schwartz JP, Taniwaki T;  
DR WPI; 96-039966/04.  
DR P-PSDB; R90287.  
PT Use of pigment epithelium derived factor - for enhancing neuronal  
PT cell survival and inhibiting glial cell proliferation, useful, e.g.  
PT in CNS cell culture or to treat neuro-degenerative diseases  
PS Disclosure; Page 100-122; 151pp; English.  
CC Pigment epithelium-derived factor (PEDF) has both neuronotrophic and  
CC gliostatic activity, making it useful in cases where neurons die  
CC quickly and glia tend to proliferate (gliosis), e.g. in CNS cell  
CC culture, in neurodegenerative diseases and in CNS injury. The  
CC neuronotrophic effect of PEDF is especially useful for enhancing  
CC survival of neuronal cell cultures intended for use in  
CC transplantation. These include cultures of human foetal brain cells  
CC and neural retina and photoreceptor cells. The gliostatic activity  
CC of PEDF can be applied to inhibiting glial cell proliferation in  
CC certain tumours. Antibodies directed against PEDF can be used for  
CC inhibiting PEDF activity or in an immunoassay for determining  
CC levels of PEDF in fluid, cellular or tissue samples e.g for  
CC determining ageing and/or other degenerative diseases.  
SQ Sequence 22481 BP; 5280 A; 5708 C; 6136 G; 5347 T;

```

Query Match          4.1%; Score 85; DB 24; Length 22481;
Best Local Similarity 82.0%; Pred. No. 4.21e-39;
Matches 109; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

b 15305 ttttgtatTTtagatagacgggtttcacatgtgcctaggctgtccaaactcc 15364
||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
p 1715 TTTTTCTTTAAATGAGATGGACTTCACTGTGTGATGAGGCTGGTCTAAACTCC 1656
||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
b 15365 cggcgtcaaggcgatccacccgccttgcgcctccaaagtgtggattacaggcgtgagcc 15424
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
p 1655 CGAGCTCAAGCAATCCACCTGCCTCAGCTCATCAAAGTGTGGATTACAGGCCATGCC 1596
||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
b 15425 accgcgcgtggcc 15437
||| | | | |
p 1595 ACCGCATGTGGCC 1583

```

RESULT 3  
ID T38689 standard; cDNA; 2477 BP.  
AC T38689;  
DT 12-JAN-1997 (first entry)  
DE Human CRTAM.  
KW Cytotoxic or regulatory T-cell associated molecule; CRTAM;  
KW physiology; cell regulation; development; differentiation;  
KW T-cell; progenitor; ss.

OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 38.1219  
FT /tag= a  
PN WO9634102-A1.  
PD 31-OCT-1996.  
PF 25-APR-1996; U05329.  
PR 26-APR-1995; US-429742.  
PA (SCHE ) SCHERING CORP.  
PI Bazan JF, Kennedy JL, Zlotnik A;  
DR WPI; 96-497634/49.  
DR P-PSDB; W04404.  
PT Cytotoxic or Regulatory T-cell associated Mol., CRTAM, - useful to  
PT develop prods. for diagnosis and treatment of conditions involving  
PT abnormal cell physiology  
PS Claim 3; Page 60-62; 74pp; English.  
CC CRTAM proteins are involved in the regulation of cellular physiology,  
CC development, differentiation or function of various cell types,  
CC including haematopoietic cells and partic. T-cell progenitors. The  
CC prods. can be used to develop prods. for the diagnosis and treatment  
CC of conditions associated with abnormal physiology or development,  
CC including abnormal proliferation, e.g. cancers, or degenerative  
CC conditions. The physiology or development of a cell can be modulated  
CC by contacting the cell with an agonist or antagonist (i.e. an anti-  
CC CRTAM peptide antibody) of a CRTAM peptide.  
SQ Sequence 2477 BP; 798 A; 527 C; 548 G; 604 T;

```

Query Match          4.0%; Score 83; DB 24; Length 2477;
Best Local Similarity 81.2%; Pred. No. 1.01e-37;
Matches 108; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db  1673 ggcacaggccggctgtgtttatgcgttaatcttagacttgggggtgggtggcaga 1732
||| ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy  1583 GGCCACATGGCTGGCTCATGCCTGTAATCCAGCACTTGATAGGCTGAGGCAGGTGGA 1642

Db  1733 tcatttgagggtcagggttggagaccaggccgtggccaaatcatgtgaaacccgtctact 1792
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy  1643 TTGCTTGAGCTCGGGAGTTGAGACCAGCCTCATCACACAGTGAACACTCCATCTCAATT 1702

Db  1793 aaaaatgcaaaaa 1805
| | | | | | | |
Qy  1703 TAAAAAAGAAAAAA 1715

```

**RESULT** 4  
ID T59650 standard; cDNA; 2562 BP.  
AC T59650;  
DT 04-MAY-1997 (first entry)  
DE Human dsRNA-dependent protein kinase cDNA.  
KW dsRNA-dependent protein kinase; PKR; 2'-5A synthetase;  
KW 2'-5A-dependent RNase; RNase L; 2'-5A system; antiviral;  
KW RNA degradation; transgenic plant; tobacco; disease resistance;  
KW crop protection; tobacco mosaic virus; tobacco etch virus;  
KW alfalfa mosaic virus; vector pAM2200; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 187..1842  
FT /\*tag= a  
PN W09639806-A1.  
PD 19-DEC-1996.  
PF 07-JUN-1996; U09895.  
PR 07-JUN-1995; US-487797.  
PA (CLEV-) CLEVELAND CLINIC FOUND.  
PI Mitra A, Silverman RH;  
DR WPI; 97-051617/05.  
DR P+PSDB; W12705.  
PT Transgenic plants co-expressing 2'-5A-dependent RNase and 2'-5A  
PT synthetase - have increased resistance to viral infection esp. 1  
PT tobacco mosaic virus, tobacco etch virus or alfalfa mosaic virus  
PS Disclosure; Page 145-146; 189pp; English.  
CC A cDNA clone (T59650) codes for human dsRNA-dependent protein  
CC kinase (PKR) (W12705), an antiviral protein that is believed to  
CC phosphorylate the alpha subunit of translation factor eIF2-alpha

CC which indirectly inhibits protein synthesis initiation. Novel  
 CC transgenic plants, such as transgenic tobacco, express (together or  
 CC alone) the PKR, human 2'-5A synthetase (see also T59645) and human  
 CC or mouse 2'-5A-dependent RNase (see also T59648-49). When the  
 CC plants are exposed to tobacco mosaic virus, tobacco etch virus and  
 CC alfalfa mosaic virus, necrotic local lesions occur instead of  
 CC typical systemic infections.  
 SQ Sequence 2562 BP; 842 A; 478 C; 501 G; 741 T;

Query Match 4.08; Score 83; DB 28; Length 2562;  
 Best Local Similarity 83.2%; Pred. No. 1.01e-37;  
 Matches 104; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 2223 ttttgtttaaaaagcagggttcacatgtggccaggctgtcaactcc 2282  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 1715 TTTTTCTTTAAATTGAGATGGAGTTCACTGTGTGATGAGGCTGGTCAACTCC 1656

Db 2283 tgacctcaagtaatccacccgcctccaaagtgtggattacaggatgagcc 2342  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 1655 CGAGCTAACGCAATCCACCTGCCTCAGCCTATCAAAGTGCTGGATTACAGGCATGAGCC 1596

Db 2343 accgc 2347  
 |||||

Cp 1595 ACCGC 1591

RESULT 5

ID T03903 standard; DNA; 2562 BP.

AC T03903;

DT 27-JAN-1996 (first entry)

DE Human p68 kinase mRNA (PKR) coding sequence.

KW PK68; p68 kinase; mrP68; ss.

OS Homo sapiens.

PN WO952245-A.

PD 24-AUG-1995.

PF 16-FEB-1995; U02058.

PR 18-FEB-1994; US-198973.

PA (CLEV-) CLEVELAND CLINIC FOUND.

PI Sengupta DN, Silverman RH;

DR WPI; 95-302493/39.

PT New transgenic plants resistant to viral infection contg. 2'-5A-dependent  
 PT RNase - useful in developing products useful in gene therapy against  
 PT viral disease and cancer.

PS Claim 4; Figure 18; 196pp; English.

CC PKR (PK68) is a lysine - arginine mutant PKR (mrPK68). The mutant  
 CC PKR protein binds to dsRNA but has no kinase activity. A transgenic  
 CC plant is claimed which includes the nts in T03903 or any part of  
 CC this sequence which contains the complete or partial coding  
 CC sequence for PKR or the ds RNA binding domain of PKR. The  
 CC translation product of the complete coding sequence for human  
 CC p68 kinase mRNA (PKR) is given in R82663.

SQ Sequence 2562 BP; 842 A; 479 C; 501 G; 740 T;

Query Match 4.08; Score 83; DB 15; Length 2562;  
 Best Local Similarity 83.2%; Pred. No. 1.01e-37;  
 Matches 104; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 2223 ttttgtttaaaaagcagggttcacatgtggccaggctgtcaactcc 2282  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 1715 TTTTTCTTTAAATTGAGATGGAGTTCACTGTGTGATGAGGCTGGTCAACTCC 1656

Db 2283 tgacctcaagtaatccacccgcctccaaagtgtggattacaggatgagcc 2342  
 ||||| ||||| ||||| ||||| ||||| |||||

Cp 1655 CGAGCTAACGCAATCCACCTGCCTCAGCCTATCAAAGTGCTGGATTACAGGCATGAGCC 1596

Db 2343 accgc 2347  
 |||||

Cp 1595 ACCGC 1591

RESULT 6

ID Q92781 standard; DNA; 3234 BP.

AC Q92781;

DT 09-DEC-1995 (first entry)  
 DE Human thymopoietin gene fragment.  
 KW Thymopoietin; diagnostic; therapeutic; gene therapy; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT exon 1..54  
 FT /\*tag= a  
 FT /note= "3' end of exon 6"  
 FT exon 1357..1445  
 FT /\*tag= b  
 FT /note= "exon 7"  
 FT exon 2572..3234  
 FT /\*tag= c  
 FT /note= "exon 8 - partial sequence"  
 PN WO9517205-A1.  
 PD 29-JUN-1995.  
 PF 13-DEC-1994; U14356.  
 PR 21-DEC-1993; US-171382.  
 PA (IMMU-) IMMUNOBIOLOGY RES INST INC.  
 PI Culler MD, Goldstein G, Harris CA, Setcavage DR;  
 PI Shenbagamurthi P, Siekierka JJ, Talle MA;  
 DR WPI; 95-240474/31.  
 PT Polynucleotide(s) encoding human thymopoietin proteins - used to  
 PT develop prods. for diagnosis and therapy involving immune or nervous  
 PT system conditions.  
 PS Disclosure; Fig 11a-11c; 85pp; English.  
 CC The sequence represents a fragment of the human thymopoietin gene,  
 CC including the 3' end of exon 6, exon 7 and a partial sequenncce for  
 CC exon 8. DNA encoding human thymopoietin, isolated from  
 CC a cDNA library prepared from human thymus RNA, may be expressed in  
 CC a host cell e.g. bacterium (preferably Escherichia coli), fungus,  
 CC insect or mammalian cell for production of recombinant thymopoietin.  
 CC Thymopoietin has a regulatory effect on the mammalian immune system,  
 CC and can be used for treating/modulating an immune or nervous system  
 CC condition, and for the treatment of chronic infection, autoimmune  
 CC disorders and certain affective psychiatric or neurological  
 CC disorders. The protein and the DNA can be used as diagnostics;  
 CC the DNA can be used in gene therapy.  
 SQ Sequence 3234 BP; 933 A; 577 C; 617 G; 1107 T;

Query Match 4.08; Score 84; DB 15; Length 3234;  
 Best Local Similarity 80.9%; Pred. No. 2.07e-38;  
 Matches 110; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 898 ttttgtttaaaaagcagggttcacatgtggccaggctgtcaactcc 957  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 1715 TTTTTCTTTAAATTGAGATGGAGTTCACTGTGTGATGAGGCTGGTCAACTCC 1656

Db 958 tgacctcaagggtatccacccgcctcagccctccaaagtgtggattacaggatgagcc 1017  
 ||||| ||||| ||||| ||||| |||||

Cp 1655 CGAGCTAACGCAATCCACCTGCCTCAGCCTATCAAAGTGCTGGATTACAGGCATGAGCC 1596

Db 1018 accgtaccggcccaa 1033  
 ||||| |||||

Cp 1595 ACCGCATGGCTAA 1580

RESULT 7

ID Q10572 standard; DNA; 1047 BP.

AC Q10572;

DT 09-APR-1991 (first entry)

DE Human Natriuretic Peptide Receptor B.

KW NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;  
 KW hyperaldosteronism; glaucoma; guanyl cyclase.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..22

FT /label= signal sequence

FT Protein 12

FT /label= mature NPBR

FT Domain 23..455

FT /label= extracellular domain

FT /note= "binds natriuretic peptides A,B and C"

Qy	521	AATCAGGTCAAACAAATAAAGTCTGTACCAACGACCA-GAGACACCGTGTGTCAGTGT	579
Db	442	dddnscdktnsnstnanvngtgntnnmngvssnnnnrknnmnknnsasmnwrnrwnnnn	501
:	::	::	::
Qy	580	GAAAAA-GGAAGCTTCAGGATAAAAACCTCCCTGAGATGTGCCGGACTGACACAGG	638
Db	502	gnsnryhkagsrsntnsnrgssygsnmtahgkynnnantghknkgnvankhvnkkrrnn	561
	::	::	
Qy	639	GTGTCCCCAGGGATGGTCAAGGTCAAGTATTGTACGCCCGGAGTCACATCAAGTGC	698
Db	562	rnvnnnnkhmrdrvnnnhntrnngacndnnncnvtncnrgsnnndnnndsnndwmnry	621
:	:: :	:	:
Qy	699	AAATGAATCAGCTGCCAGTTCACTGGAAAACCCCAGCAGCGGAGGAGACAGTGACCAC	758
Db	622	snnn-dnvkgmannhsnnsshgsnksscnvvdssrnvnkntdygnasnrstanndnnn	680
:	::	:	:
Qy	759	CATCTGGGGATGCCTGCCTCCATCACTACCTTATCATAGTAGGTTTAGTCAT	818
Db	681	yakknnntnnnsgnnnnttgmaadivysngnnnnnnarsgnnyngndnsnknnvky	740
:	::	:	:
Qy	819	CATTTAGCTGTGGTTGTGGTTGGCTTTCATGTCGGAAGAAATTCTACCTACCTCAA	878
Db	741	rngrnrynrnsndrtnnnnnnvnmmrncrwandnanrnrdngnnkgnrrrankngtssndn	800
:	::	:	:
Qy	879	AGGCATCTGCTCAGGTGGAGGAGTCCGGAACGTGTGCACAGACTCTT-TCCGGC	937
Db	801	nnrrmnyyannnnknvnrrtnaynnkrkanannnnnhsvannnkrgntvnanandsv	860
:	::	:	:
Qy	938	GGCGTTCATGTCTTACAGACTTCCAGCTGGCCGGAGGACAATGCCCGAACGAGACCTGA	997
Db	861	tynnsdnvgntansanstnmvvtnnnndnytcndannndnvykvntngdaymvvsgnn	920
:	::	:	:
Qy	998	GTAACAGATACTTGCAGCCCACC-CAGGTCTGTAGACGAGGAAATCCAAGTCAGGAGCTG	1056
Db	921	rngrhannnarmananndavssnrrnhrnhdnrrngrvhtgnvcagvvnkmnrycnn	980
:	::	:	:
Qy	1057	GCAGAGCTAACAGGTGTACTGTAGAGTGYGCCAGAGGACCAACGCCGCTCTGCAACAG	1116
Db	981	gdtvntasrmnsngnankhnvsstkddandnngc	1014
	:	:	:
Qy	1117	GCAGAAGCTGAAGGGTGTAGAGGAGGAGGCTG	1150

RESULT 8

ID Q10572 standard; DNA; 1047 BP.  
AC Q10572;  
DT 09-APR-1991 (first entry)  
DE Human Natriuretic Peptide Receptor B.  
KW NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;  
KW hyperaldosteronism; glaucoma; guanyl cyclase.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..22  
FT /label= signal sequence  
FT Protein 12  
FT /label= mature NPBR  
FT Domain 23..455  
FT /label= extracellular domain  
FT /note= "binds natriuretic peptides A,B and C]"  
FT Domain 456..456  
FT /label= transmembrane domain  
FT Domain 479..1047  
FT /label= cytoplasmic domain  
FT /note= "GC and protein kinase activity"  
FT Modified -site 24..26  
FT /label= N-glycos\_site  
FT Modified -site 35..37  
FT /label= N-glycos\_site  
FT Modified -site 161..163  
FT /label= N-glycos\_site  
FT Modified -site 195..197  
FT /label= N-glycos\_site  
FT Modified -site 244..246

FT /label= N-glycos\_site  
 FT Modified -site 277..279  
 FT /label= N-glycos\_site  
 FT Modified -site 349..351  
 FT /label= N-glycos\_site  
 FT Modified -site 600..602  
 FT /label= N-glycos\_site  
 PN WO9100292-A.  
 PD 10-JAN-1991.  
 PF 22-JUN-1990; U03586.  
 PR 23-JUN-1989; US-370673.  
 PA (GETH ) GENENTECH INC.  
 PI Chang M, Goeddel D, Lowe D;  
 DR WPI; 91-036711/05.  
 DR N-PSDB; Q10324.  
 PT Natriuretic protein receptor B - for diagnosis and treatment of  
 kidney failure, heart failure, hyperaldosteronism, glaucoma etc.  
 PS Claim 3; Fig 1; 49pp; English.  
 CC The sequence was derived from the DNA encoding natriuretic peptide  
 receptor B, NPRB, having guanyl cyclase (GC) activity and protein  
 kinase activity. The DNA can be inserted into expression vectors  
 for the prodn. of the protein, opt. after being mutated to produce  
 NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=  
 114,952). The protein (or variants) can be used in treatment of  
 natriuretic peptide disorders, and also to isolate peptides using  
 affinity chromatography. Antibodies with affinity for NPRB can  
 also be prepd.  
 SQ Sequence 1047 BP; 87 A; 15 C; 83 G; 51 T;

Query Match 3.9%; Score 82; DB 2; Length 1047;  
 Best Local Similarity 9.8%; Pred. No. 4.96e-37;  
 Matches 100; Conservative 287; Mismatches 618; Indels 15; Gaps 15;

Db 17 vrrnngarnntnavvnnnhnnsiyawawnrvgnavanavanngrannvdnrnvssnnngacs 76  
 :: | : : : : : : : : | : | : : : : |  
 Cp 1197 CAGCAAGGTGCTGATGTCAGCGGAGTCAGCCTATTCACTGGAACCCAGCAGCCTCCT 1138  
 Db 77 nynannsadvdknyhdndnnngngcvynaasvarnashwrnnntagavasgnsa-kndh 135  
 : | : : : : | : | : | : : : | : | : : : |  
 Cp 1137 CTGACACCCTTCAGCTCTGCCCTTCCA-GCAGACCGCTGGCTCCTCTGGRACTCTA 1079  
 Db 136 yrtnvrtngsankngnnvvtvhghnnwrtaraannyndartddrnhyntngvnnangsn 195  
 :: | : : : : | : : | : : | : : | : | : |  
 Cp 1078 CAGTCACACCTGTTAGCTCTGCCAGCTCTGACCTGGATTCTGTCAGAGACCTGGG 1019  
 Db 196 nsvhnhvyyarnnggnnnathnnrangrnyvngcnmnnhnnnnnanrnnntngdyvnnyn 255  
 :: | : : : | : | : | : | : | : | : | : |  
 Cp 1018 TGGGCTGCAAGTATCTGTTACTCAGGGTCT-CGTTGGGGCATTCCTCCGCCAGGA 960  
 Db 256 dvngnsnragntratgrnwndnrtrnnananrnanntvvntrvnnnnnnnnnnnnnn 315  
 :: | | | : | : | | : | : | : | : | : |  
 Cp 959 ACTCGTGAAGGACATGAACGCCCGAAAAGGAC-TCTGTGCACACGTTGGACCTCC 901  
 Db 316 rarndngvnnngnsnmnnnagcnynnnyanvnnntnnngtrndgnrnvnkmngrryhg 375  
 : | : | : | : | : | : | : | : | : | : |  
 Cp 900 TCCACCACTGAGCAGATGCCCTTGAGGTAAGAAATGAATTCTCCGACATGAAAAGCC 841  
 Db 376 vtgnvymdknnndrtdnvnwamgdndsgdnnaahysganknnwwtgrnnnnvkgannsd 435  
 : | : : | : | : | : | : | : | : | : | : | : |  
 Cp 840 AACCAACAACAGCTAA-AATGATGACTAAACCACTATGATGATAAGGTAGTGTAGG 782  
 Db 436 nnncandndnsdcdtnnstnanvngtgtnnmngyssnnnnrknmnknnsmnwrrn 495  
 | : | : | : | : | : | : | : | : | : | : |  
 Cp 781 GAG-AGGCCAA-GCATCCCCAG-GATGGTGGTCACTGTCCTCCGCTGGGGTTTCC 725  
 Db 496 wnnnnngnsnryhkgagsrntsnrgs-sygsnmtahgkynnnantghknvnnvkhv 554  
 : | : | : | : | : | : | : | : | : | : | : |  
 Cp 724 CAGTGGAACTGGCAGCTGATTCTTGCACCTGATGTCACCGGGGGTACAAATTAC 665  
 Db 555 kkrnnntrnvnnnnkhmrdrvnnnhtrnnga-cndnnnncnvtnycnrgsnndnnndsn 613  
 : | : | : | : | : | : | : | : | : | : | : |  
 Cp 664 TGACCTTGACCATCCCTCTGGACACCCCTGTCTACACGTCGGCACATCTCAGGGGAGT 605

Db 614 nnndwmnrysnnndnvkgmannhnsnnshgsnkssncvvdsvrnvnkntdygnasrnstan 673  
 :: | : : : : : : : | : : | : : | : : | : : |  
 Cp 604 TTTTATCCTGGAAGCTCCTTTTCACACTGACACACGGTGTCTGGTCGTGGTAC-AG 546  
 Db 674 nddnnyaknntannnnsgnnnttgmaadyv-sngnnnnnnarlsqgnnyngndns 732  
 :: | : | : | : | : | : | : | : | : | : |  
 Cp 545 GAACTTTATTTGTTGACCTGATTTACAAACTGTACATAGCAGGCCAGAAAGGCAAATTG 486  
 Db 733 nknnvnkvrvnqnqrnynrnsndrtnnnnnvnnmrcwandnanrndgnnkgnrrnnkn 792  
 : | : | : | : | : | : | : | : | : | : |  
 Cp 485 TTGGAAGCAATGGTGAATCCACACCCCTGTGACGGGTACAGGCTCCAGTATATTCT 426  
 Db 793 ggttsnnnnnnrmnnnyannnnknvnnrtnaynnkrkanannnnhsvannnnkrntv 852  
 | | : | : | : | : | : | : | : | : | : |  
 Cp 425 GATCTATGAGATCCTGCTGGACACTCCCTCCTGGAGGCTGCGCCTGTTGCTGTGGG 366  
 Db 853 nanandsvtnynsndnvgnntansanstnmnvvttnndnytcndanndndvykvntngday 912  
 | : | : : | | : | : | : | : | : | : | : |  
 Cp 365 GCCACTG-TCTGCTGGGGACTTCTGCTCTGCCGGGGATGGTGGCAGAGTCAACCGGAC 307  
 Db 913 mvsqnnrqngrnhrannnarmanndavssnrrhrnhdnnrrnrvgnvhnvgvvn 972  
 :: | : | : | | : | : | : | : | : | : | : |  
 Cp 306 CGGCAGC-A-GAACCGCGACGATGAACACGACGAACTAAGGATCTGGGTCCAGGAC 249  
 Db 973 kmnrycngdtvntasrmsnsnanknhvssstkdandnngcnnnnrgdvnmkkgkmr 1032  
 : | : | : | : | : | : | : || : | : | : | : |  
 Cp 248 CATGGTCTGGTCTCCGACCTGCTCTGGATAGGCCCTGCTCGAGGCCCTCGAG 189

RESULT 9  
 ID Q46958 standard; cDNA; 1618 BP.  
 AC Q46958;  
 DT 25-JAN-1994 (first entry)  
 DE Human cytokine synthesis inhibitory factor clone pH15C.  
 KW Mammalian cytokine synthesis inhibitory factor; CSIF; interleukin 10;  
 KW IL-10; immune system imbalance; human T cell; Leischmaniasis;  
 KW rheumatoid arthritis; systemic lupus erythematosus; thyroiditis;  
 KW myasthenia gravis; insulin-dependent diabetes mellitus; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 31..567  
 FT /\*tag= a  
 FT mat\_peptide 85..564  
 FT /\*tag= b  
 FT /product= mature\_CSIF  
 PN US5231012-A.  
 PD 27-JUL-1993.  
 PF 28-JUN-1989; 372667.  
 PR 28-JUN-1989; US-372667.  
 PR 20-DEC-1989; US-453951.  
 PR 06-AUG-1990; US-546235.  
 PR 20-JUL-1992; US-917806.  
 PA (SCHE ) SCHERING CORP.  
 PI Bond MW, Moore KW, Mosmann TR, Vieira PJM;  
 DR WPI; 93-249726/31.  
 DR P-PSDB; R39714.  
 PT Genes and proteins encoding cytokine synthesis inhibitory factors  
 PT - useful in treating diseases associated with cytokine  
 PT imbalances, e.g. parasitic infections and auto-immune disorders  
 PS Claim 1; Fig 4; 23pp; English.  
 CC A human T cell cDNA library was screened with probes based on the  
 CC murine CSIF gene. Two clones carrying plasmids pH5C and pH15C were  
 CC identified. (These two expression vectors are claimed). The CSIF  
 CC polypeptide they encode inhibits synthesis of cytokines associated  
 CC with delayed type hypersensitivity responses. CSIF (also called IL-  
 CC 10) can be used to treat diseases associated with cytokine  
 CC imbalances, such as leishmaniasis and MHC-associated autoimmune  
 CC diseases caused by excessive production of interferon-gamma, e.g.  
 CC rheumatoid arthritis, SLE, IIDD, myasthenia gravis and thyroiditis.  
 SQ Sequence 1618 BP; 463 A; 367 C; 356 G; 432 T;

Query Match 3.9%; Score 81; DB 7; Length 1618;  
 Best Local Similarity 79.1%; Pred. No. 2.42e-36;

Matches 110; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
Db 1168 gttctaggccggcgccgtggctcacgcctgtatccacgacttggggctgaggcg 1227  
||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 1577 GTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCAGCACTTGTAGGCTGAGGCA 1636  
Db 1228 ggtggatcacttgaggtcaggagttctaaaccagccgttcaacatggtaaaacccgtc 1287  
||| ||||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 1637 GGTGGATTGCTTGAGCTCGGGAGTTGAGACCAGCCTCATCAACACAGTGAAACTCCATC 1696  
Db 1288 tctactaaaataaaaaaa 1306  
||| ||| ||||| |||||  
Qy 1697 TCAATTAAAAAGAAAAAA 1715

## RESULT 10

ID Q10207 standard; cDNA; 1618 BP.

AC Q10207;

DT 19-MAR-1991 (first entry)

DE pH15C insert containing Human cytokine synthesis inhibitory factor.

KW Delayed-type hypersensitivity; DTH; leishmaniasis; parasite; MHC-associated autoimmune disease; interferon-gamma; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 33..566

FT /\*tag= a

PN EP-405980-A.

PD 02-JAN-1991.

PF 28-JUN-1990; 307091.

PR 28-JUN-1989; US-372667.

PR 20-DEC-1989; US-453951.

PA (SCHERING CORP.

PI Mosmann TR, Moore KW, Bond MW, Vleira PJM;

DR WPI; 91-009290/02.

DR R-PSDB; R10158.

PT Mammalian cytokine synthesis inhibitory factors - capable of inhibiting synthesis of cytokine(s) associated with delayed-type

PT hypersensitivity and useful in treatment of e.g. leishmaniasis

PS Disclosure; Fig 4; 31pp; English.

CC The gene product may be used in treatment of diseases associated

CC with MHC-linked immune response, supressing a cell mediated or

CC humoral immune response. It may specifically be used to treat

CC delayed-type hyper-sensitivity, leishmaniasis, and immune disorders.

SQ Sequence 1618 BP; 461 A; 369 C; 356 G; 432 T;

Query Match 3.9%; Score 81; DB 2; Length 1618;

Best Local Similarity 79.18; Pred. No. 2.42e-36;

Matches 110; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 1168 gttctaggccggcgccgtggctcacgcctgtatccacgacttggggctgaggcg 1227  
||| ||||| ||| ||| ||| ||| ||| ||| |||  
Qy 1577 GTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCAGCACTTGTAGGCTGAGGCA 1636  
Db 1228 ggtggatcacttgaggtcaggagttctaaaccagccgttcaacatggtaaaacccgtc 1287  
||| ||||| ||| ||| ||| ||| ||| ||| |||  
Qy 1637 GGTGGATTGCTTGAGCTCGGGAGTTGAGACCAGCCTCATCAACACAGTGAACTCCATC 1696  
Db 1288 tctactaaaataaaaaaa 1306  
||| ||| ||||| |||||  
Qy 1697 TCAATTAAAAAGAAAAAA 1715

## RESULT 11

ID Q44278 standard; DNA; 17327 BP.

AC Q44278;

DT 24-NOV-1993 (first entry)

DE Serglycin - proteoglycan peptide core.

KW Haematopoietic cell secretory granule proteoglycan;

KW positive; negative; transcriptional regulatory element;

KW enhancer; eukaryotic promoter; constitutive suppressor;

KW TATA-box; ss.

OS Homo sapiens.

FH Key Location/Qualifiers  
FT misc\_signal 373..621  
FT /\*tag= a  
FT /note= "5' regulatory region;  
FT claim 1-3, page 78"  
FT misc\_signal 373..433  
FT /\*tag= b  
FT /note= "negative transcriptional regulatory element;  
FT claim 6 and 9-10, page 78-79"  
FT enhancer 514..541  
FT /\*tag= c  
FT /note= "enhancer transcriptional regulatory element;  
FT claim 11 and 14-15, page 79"  
FT promoter 582..602  
FT /\*tag= d  
FT /note= "eukaryotic promoter element;  
FT claim 16 and 19-20, page 80"  
FT CDS 675..16646  
FT /\*tag= e  
FT /label= serglycin  
FT exon 622..753  
FT /\*tag= f  
FT /number= 1  
FT exon 9597..9744  
FT /\*tag= g  
FT /number= 2  
FT exon 16397..17327  
FT /\*tag= h  
FT /number= 1  
FT sig\_peptide 675..9598  
FT /\*tag= i  
FT /note= "interrupted by exon 1"  
FT misc\_RNA 16449..16502  
FT /\*tag= j  
FT /note= "serine-glycine rich glycosaminoglycan  
FT attachment region"  
FT polyA\_signal 17062..17067  
FT /\*tag= k  
FT misc\_difference 6135  
FT /\*tag= l  
FT /note= "base represented as N in the specification"  
PN W09313119-A.  
PD 08-JUL-1993.  
PF 23-DEC-1992; U11194.  
PR 03-JAN-1992; US-816289.  
PR 02-JUL-1992; US-906871.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
PI Avraham S, Stevens RL;  
DR WPI; 93-227261/28.  
DR P-PSDB; R39393.  
PT Transcription regulatory elements of ser-glycin gene - specific  
PT for haematopoietic cells, also trans-acting transcriptional  
PT binding factors  
PS Disclosure; Fig 4B-J; 112pp; English.  
CC A negative transcription regulatory element (a constitutive  
CC suppressor) between residues -250 and -190 (see tag b) of the 5'  
CC flanking region of the human serglycin gene, a positive  
CC (hematopoietic cell enhancer) regulatory element located between  
CC residues -118 and -81 (see tag c), an equiv. of the TATA-box and  
CC a novel eukaryotic promoter that utilises such equiv. (see tag d)  
CC are identified. The regulatory elements, vectors and hosts  
CC provided with these elements, are useful in the control of gene  
CC transcription of heterologous genes in eukaryotic cells, esp.  
CC hematopoietic cells.

SQ Sequence 17327 BP; 4936 A; 3604 C; 3741 G; 5045 T;

Query Match 3.9%; Score 82; DB 7; Length 17327;

Best Local Similarity 83.18; Pred. No. 4.96e-37;

Matches 103; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 11013 gccaggtggggctcatgcctgtatccacgacttggggccggaggcgaggat 11072  
||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 1584 GCCACATGCGGTGGCTCATGCCTGTAATCCAGCACTTGTAGGCTGAGGAGGTGGAT 1643

Db 11073 tgtttgccaggatggccagcctggcaacatgtgagaccatatcttattt 11132  
   ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Qy 1644 TGCTTGAGCTGGGAGTTGAGACCAGCCTCATCAACACAGTGAACACTCCATCTCAATT 1703  
 Db 11133 caaa 11136  
   |||  
 Qy 1704 AAAA 1707

RESULT 12  
 ID Q60835 standard; DNA; 429 BP.  
 AC Q60835;  
 DT 16-MAR-1994 (first entry)  
 DE Human brain Expressed Sequence Tag EST01613.  
 KW Gene transcription product; genetic markers; tagging; in vivo;  
 KW transcription; mapping; locations; chromosomes; chromosomal; ss.  
 OS Homo sapiens.  
 PN W09316178-A.  
 PD 19-AUG-1993.  
 PR 12-FEB-1993; U01294.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
 PI Adams MD, Moreno RF, Venter CJ.  
 DR WPI; 93-272882/34.  
 PT Enriched oligonucleotides and corresp. sequences - used as  
 PT markers for human genes transcribed in-vivo, facilitate tagging  
 PT of most human genes  
 PS Example 4; Page 398; 500pp; English.  
 CC The Expressed Sequence Tag was isolated from a human brain cDNA  
 CC library as part of a large set of ESTs which can be used as markers  
 CC for human genes transcribed in vivo. They can be used to facilitate  
 CC tagging of most human genes, for mapping locations of expressed genes  
 CC on chromosomes, for individual or forensic identification, for mapping  
 CC locations of disease-associated genes, for identification of tissue  
 CC type, and for prepn. of antisense sequences, probes and constructs.  
 CC EST01613 has a "poor" coding probability as evaluated using the  
 CC coding-region prediction program CRM. See also Q59041-Q61440.  
 SQ Sequence 429 BP; 140 A; 87 C; 99 G; 100 T;

Query Match 3.8%; Score 80; DB 8; Length 429;  
 Best Local Similarity 79.1%; Pred. No. 1.18e-35;  
 Matches 106; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 99 ggccgggtgttgtgnctcatgcctgtatcccacgtttggggctgggggtgg 158  
   ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Qy 1583 GGCCACATGCGGTGGCTCATGCCCTGTAATCCCACACTTGTAGGCTGAGGCAGGTGGA 1642  
 Db 159 tcacttgaggctcaggagttcgagaccagccatggccaaacatggcgg 218  
   ||||| ||||| ||||| ||||| |||||  
 Qy 1643 TTGCTTGAGCTCGGGAGTTGAGACCAAGCAGCCTCATCAACACAGTGAACACTCCATCTCAATT 1702  
 Db 219 aaaaataaaaaaaa 232  
   ||||| |||||  
 Qy 1703 TAAAAAGAAAAAAA 1716

RESULT 13  
 ID T03731 standard; cDNA; 1830 BP.  
 AC T03731;  
 DT 26-MAR-1996 (first entry)  
 DE TNF-R p75IC-binding protein 75.3 partial cDNA.  
 KW Tumour necrosis factor receptor; TNF-R; p75IC;  
 KW intracellular domain binding protein; human immunodeficiency virus;  
 KW HIV; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT misc\_difference 354  
 FT /\*tag= a  
 FT /note= "base n at position 354 is not identified  
 FT in the specification"  
 FT misc\_difference 430  
 FT /\*tag= b

FT /note= "base n at position 430 is not identified  
 FT in the specification"  
 FT misc\_difference 438  
 FT /\*tag= c  
 FT /note= "base n at position 438 is not identified  
 FT in the specification"  
 FT misc\_difference 544  
 FT /\*tag= d  
 FT /note= "base n at position 544 is not identified  
 FT in the specification"  
 FT misc\_difference 677  
 FT /\*tag= e  
 FT /note= "base n at position 677 represents an  
 FT undetermined sequence of unknown length"  
 FT misc\_difference 682  
 FT /\*tag= f  
 FT /note= "base n at position 682 is not identified  
 FT in the specification"  
 FT misc\_difference 729  
 FT /\*tag= g  
 FT /note= "base n at position 729 is not identified  
 FT in the specification"  
 FT variation 743  
 FT /\*tag= h  
 FT /note= "base n at position 743 is not identified  
 FT in the specification"  
 FT misc\_difference 762  
 FT /\*tag= i  
 FT /note= "base n at position 762 is not identified  
 FT in the specification"  
 FT misc\_difference 779  
 FT /\*tag= j  
 FT /note= "base n at position 779 is not identified  
 FT in the specification"  
 PN W09531544-A1.  
 PD 23-NOV-1995.  
 PF 11-MAY-1995; U05854.  
 PR 11-MAY-1994; IL-109632.  
 PR 02-OCT-1994; IL-111125.  
 PA (WEIN/) WEINWURZEL H.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Boldin M, Mett I, Varfolomeev E, Wallach D;  
 DR WPI; 96-010930/01.  
 PT TNF-NGF receptor superfamily intracellular domain-binding proteins -  
 PT useful for modulating receptor function, e.g. for treating tumours  
 PT or HIV-infected cells  
 PS Claim 13; Fig 1b; 96pp; English.  
 CC A cDNA clone (T03731) coding for a portion of novel human protein  
 CC 75.3 was obtnd. from HeLa cDNA by yeast 2-hybrid analysis. 75.3 is  
 CC capable of binding the intracellular domain of tumour necrosis factor  
 CC receptor (TNF-R) protein p75. The cDNA can be used to produce 75.3  
 CC (or fusion proteins including 75.3) in transformant host cells for  
 CC use in modulating TNF-R activity as a means of treating tumours or  
 CC e.g. HIV-infected cells.  
 SQ Sequence 1830 BP; 604 A; 349 C; 384 G; 483 T;

Query Match 3.8%; Score 79; DB 17; Length 1830;  
 Best Local Similarity 82.1%; Pred. No. 5.73e-35;  
 Matches 101; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
 Db 89 ggtggctatgcctgtatcccacgtttggggctggggatgcctaagc 148  
   ||||| ||||| ||||| |||||  
 Qy 1593 GGTGGCTCATGCCCTGTAATCCCACATTGTAGGCTGAGGCAGGTGGATTGCTTGAGC 1652  
 Db 149 ccaggatgttgcacatgcgcctggcaacatggtaaacccatctctacaaaaatgc 208  
   ||||| ||||| ||||| ||||| |||||  
 Qy 1653 TCGGGAGTTGAGACCAGCAGCCTCATCAACACAGTGAACACTCCATCTCAATTAAAAAGAAA 1712  
 Db 209 aaa 211  
   |||  
 Qy 1713 AAA 1715

RESULT 14

ID Q75209 standard; cDNA; 8342 BP.

AC Q75209;

DT 23-AUG-1995 (first entry)

DE ALL-1 (acute lymphocytic leukaemia-1) breakpoint cluster region.

KW Acute lymphoblastic leukaemia; acute nonlymphoblastic leukaemia;

KW chromosomal translocation; abnormality; detection; rearrangement;

KW breakpoint cluster region; Alu repeat; chromosome 11; probe B859; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT exon 1..263

FT /\*tag= a

FT /number= 5

FT intron 264..2352

FT /\*tag= b

FT exon 593..666

FT /\*tag= c

FT /number= 6

FT intron 667..798

FT /\*tag= d

FT repeat\_unit 799..1108

FT /\*tag= e

FT /rpt\_type= OTHER

FT /note= "Alu repeat-a (Class J)"

FT repeat\_unit 1119..1420

FT /\*tag= f

FT /rpt\_type= OTHER

FT /note= "Alu repeat-b (Class Sx)"

FT repeat\_unit 1432..1716

FT /\*tag= g

FT /rpt\_type= OTHER

FT /note= "Alu repeat-c (Class Sb0)"

FT repeat\_unit 1921..2216

FT /\*tag= h

FT /rpt\_type= OTHER

FT /note= "Alu repeat-d (Class J)"

FT exon 2353..2484

FT /\*tag= i

FT /number= 7

FT intron 2485..3031

FT /\*tag= j

FT exon 3032..3145

FT /\*tag= k

FT /number= 8

FT intron 3146..6787

FT /\*tag= l

FT repeat\_unit 3973..4268

FT /\*tag= m

FT /rpt\_type= OTHER

FT /note= "Alu repeat-e (Class Sb0)"

FT repeat\_unit 4764..5094

FT /\*tag= n

FT /rpt\_type= OTHER

FT /note= "Alu repeat-f (Class J)"

FT repeat\_unit 6072..6362

FT /\*tag= o

FT /rpt\_type= OTHER

FT /note= "Alu repeat-g (Class S)"

FT exon 6788..6934

FT /\*tag= p

FT /number= 9

FT intron 6935..7966

FT /note= "nucleotides 7429-7559 show about 80% sequence identity to genomic sequences found in 5' regulatory regions, 3' segments, or in introns of several genes such as ApoA4, Factor VIIc subunit and G6PD"

FT /\*tag= q

FT repeat\_unit 7164..7427

FT /\*tag= r

FT /rpt\_type= OTHER

FT /note= "Alu repeat-h (Class Sx)"

FT exon 7967..8062

FT /\*tag= s

FT /number= 10

FT intron 8063..8303

FT /\*tag= t

FT exon 8304..8342

FT /\*tag= u

FT /number= 11

FT PN WO9426930-A.

FT PD 24-NOV-1994.

FT PF 22-APR-1994; U04496.

FT PR 14-MAY-1993; US-062443.

FT PA (UYJE-) UNIV JEFFERSON THOMAS.

FT PI Canaani E, Croce C;

FT DR WPI; 95-006818/01.

FT DR P-PSDB; R66467.

FT PT New acute lymphocytic leukaemia gene prods. - used for the diagnosis and treatment of leukaemias, partic. acute lymphoblastic or nonlymphoblastic leukaemia

FT PS Example 5; Fig 22; 207pp; English.

CC A phage clone, mg11.1, which spans the breakpoint cluster region in the ALL-1 gene has been sequenced (Q75209). Eight Alu repeat sequences were identified and classified based on criteria published in Milosavljevic et al. (J.Mol.Evol. 32, 105-121, 1991). The high concentration of Alu sequences within the area spanned by exons 6 and 7 suggested a possible role for Alu in the chromosomal translocations involving the ALL-1 gene. Homologous recombination is not involved so the Alu repeats may act indirectly by destabilising the region.

SQ Sequence 8342 BP; 2604 A; 1613 C; 1758 G; 2367 T;

Query Match 3.8%; Score 79; DB 13; Length 8342;  
Best Local Similarity 81.1%; Pred. No. 5.73e-35;  
Matches 103; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Db 4771 tgcatggctcacgcctgtatccagttttggaggctgacgcaggaggaccgctt 4830  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 1590 TGCCTGGCTCATGCCTGTAAATCCCAGCACITTGATAGGCTGAGGCAGGTGGATTGCTT 1649

Db 4831 agtcaggaggtaagaccaggcctgagcaccatagtgagacctatctactaaaaaaa 4890  
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 1650 AGCTCGGGAGTTTGAGACCAAGCCTCATCACACAGTGAACACTCCATCTCAATTAAAAAG 1709

Db 4891 aaataaaa 4897  
||| |||||  
Qy 1710 AAAAAAAA 1716

RESULT 15

ID T16333 standard; DNA; 8391 BP.

AC T16333;

DT 29-JUL-1997 (revised)

DT 06-JUN-1996 (first entry)

DE MLL gene 8.3 kb fragment encoding all common translocation breakpoints.

KW MLL; myeloid; lymphoid; leukaemia; probe; chromosome; translocation;

KW mutation; 11q23; lymphoma; monitoring; ss.

OS Homo sapiens.

PN US5487970-A.

PD 30-JAN-1996.

PF 17-JUN-1992; 900689.

PR 17-JUN-1992; US-900689.

PR 16-DEC-1992; US-991244.

PR 17-JUN-1993; US-080255.

PA (ARCH-) ARCH DEV CORP.

PI Diaz MO, Rowley JD;

DR WPI; 96-105221/11.

PT Detection of 11q23 chromosome translocation(s) - using myeloid/lymphoid leukaemia nucleic acid probes, for diagnosis and monitoring of leukaemia(s) and lymphoma(s)

PT PS Example 3; Column 49-56; 47pp; English.

CC T16333 is an 8.3 kb human genomic DNA BamHI fragment of the human MLL (myeloid/lymphoid leukaemia) gene. This sequence contains all of the common MLL translocation breakpoints and may be used to map the intron-exon boundaries within this region and to identify the

WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
High quality sequence stops: 249  
Source: IMAGE Consortium LILN  
This clone is available royalty-free through LILN ; contact the  
IMAGE Consortium (info@image.liln.gov) for further information.  
FEATURES  
Location/Qualifiers  
1. 407  
/organism="Homo sapiens"  
/clone="150393"  
BASE COUNT  
ORIGIN  
90 a 104 c 97 g 111 t 5 others

ORIGIN  
Query Match 4.2%; Score 87; DB 12; Length 407;  
Best Local Similarity 83.2%; Pred. No. 6.15e-107;  
Matches 109; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
Matches 109;  
Db 135 TTTTGTATTTTACTAGAGATGGATTTCACCATGTTGCCAGCTGCTCAACTCC 194  
Cp 1715 TTTCITCTTTAAATTGAGATGGATTTCACGTGTTGATGAGCTGGTCARACTCC 1656  
Db 195 TGAACCTCAAGTCACTGATCACCTGCTCAGCCTCCAAAGTGTGATTACAGTGAGCC 254  
Cp 1655 CGAGGTCAAGCATCATACTCACCTGCTCAGCCTATCAAAGTGTGATTACAGGATGAGCC 1596  
Db 255 ACCGCACCTGG 265  
Cp 1595 ACCGATGTGG 1585

Search completed: Fri May 15 18:55:40 1998  
Job time : 1929 secs.